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The research reported here was financed in part
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Research and Development Program and by the USDA
Forest Service, Intermountain Forest and Range Experi-
nent Station.

RESEARCH SUMMARY

This paper documents a computer model designed to simulate stand development in stands affected by the Douglas-fir tussock moth. The simulation model is actually a combination of two independently developed models: the Stand Prognosis Model and the Douglas-fir Tussock Moth Outbreak Model. This Combined Model can be used to assess the likely consequences of both silvicultural treatments and tussock moth control activities for stands in the Northern Rocky Mountains, using existing forest inventories. It can be used as a tool for long-range timber management planning because it displays the projected results of alternative strategies for the management of forests affected by the tussock moth. This integrated approach permits direct comparisons of various management and tussock moth control strategies in terms of stand volume development over time, rather than an intermediate effect such as defoliation. The flexibility of the model has also proved valuable in examining the importance and sensitivity of various assumptions in the Combined Model, and thus is useful in pointing out future research needs.

This paper covers four major areas: (1) an overview and brief discussion of the Combined Stand Prognosis and DFTM Outbreak Model is given; (2) a description of the information needed to use the Combined Model is given, which includes documentation and discussion of the input options; (3) the output and information produced by the Combined Model is discussed; and (4) numerous examples are presented that illustrate the behavior and sensitivity of the Combined Model when major input options are varied.

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United States
Department of
Agriculture

Forest Service

**Intermountain
Forest and Range
Experiment Station
Ogden, UT 84401**

General Technical
Report INT-127

September 1982

A User's Guide to the Combined Stand Prognosis and Douglas-fir Tussock Moth Outbreak Model

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INTRODUCTION

This paper reports on a computer model designed to simulate stand development in forest stands affected by the Douglas-fir tussock moth (DFTM), *Orgyia pseudotsugata* (McDunnough), which is a defoliator of true firs, *Abies* spp., and inland Douglas-fir, *Pseudotsuga menziesii* var. *glauca* (Beissn.) Franco. The simulation model is actually a combination of two independently developed models: the Stand Prognosis Model (Stage 1973; Wykoff et al. 1982), and the DFTM Outbreak Model (Overton and Colbert 1976 et seq.; Colbert et al. 1979, 1981[1]; Overton et al. 1981[2]). The Stand Prognosis Model was developed by the Intermountain Forest and Range Experiment Station in Moscow, Idaho. The DFTM Outbreak Model was developed jointly by Oregon State University and the Pacific Northwest Forest and Range Experiment Station in Corvallis, Oreg. (see Colbert [1978] for a short history of the development of the Outbreak Model). The effort that resulted in the combining of these models was sponsored by the Expanded Douglas-fir Tussock Moth Research and Development Program.

Purpose

Specifically, the purpose of this paper is fourfold:
- to provide an overview and brief discussion of the Combined Stand Prognosis and Douglas-fir Tussock Moth Outbreak Model;
- to describe the information needed to use the Combined Model, including documentation of the program options and a description of program input;
- to discuss the output and information produced by the Combined Model; and
- to provide examples that illustrate the behavior and sensitivity of the Combined Model when major input options are varied.

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[1]Colbert, J. J., W. S. Overton, and C. White. 1981. Behavior of the Douglas-fir tussock moth outbreak population model. 61 p. Manuscript in process and on file at Pac. Northwest For. and Range Exp. Stn., Corvallis, Oregon.

[2]Overton, W. S., B. E. Wickman, and R. R. Mason. 1981. Nature, organization, and content of a model for population outbreaks of the Douglas-fir tussock moth. 104 p. Manuscript in process and on file at Pac. Northwest For. and Range Exp. Stn., Corvallis, Oregon.

OVERVIEW OF THE COMBINED MODEL

The Combined Stand Prognosis/DFTM Outbreak Model can be used to assess the likely consequences of both silvicultural treatments and tussock moth control activities for stands in the Northern Rocky Mountains (northern Idaho, western Montana, eastern Washington, northeastern Oregon), using existing forest inventories. It can be used as a tool for long-range timber management planning, because it displays the projected results of alternative strategies for the management of forests affected by the tussock moth. This integrated approach permits direct comparisons of various management and tussock moth control strategies in terms of stand volume development over time, rather than an intermediate effect such as defoliation. The flexibility of the model has also proved valuable in examining the importance and sensitivity of various assumptions in the Combined Model (for example, the allocation of first instar larvae to trees of various sizes), and thus is useful in pointing out future research needs.

One of the obvious advantages of a simulation model such as this is that the user can quickly and quite cheaply compare the effectiveness of rather expensive control strategies and management alternatives. Pest control strategies available to the user include simulated application of either biological or chemical controls at various phases of the outbreak; chemical control can be applied to any instar, in any phase, at any efficacy. Silvicultural management options are available for simulating partial cuttings, thinnings, changes in species composition, and the salvage of defoliated trees. In addition, the model can be used to estimate critical insect population levels above which a given control strategy (such as applying a virus) becomes practical (Mason and Torgersen 1978). Pest monitoring can then concentrate on whether or not this critical insect level is likely to be exceeded.

Even if pest control is not anticipated, the Combined Model can be a useful tool for examining the expected long-term volume yields in the face of single or multiple outbreaks of tussock moth (see figure 1). Basing harvest schedules (e.g., Stage et al. 1980) on yields anticipated from the "no outbreak" curve in figure 1 will result in suboptimal long-range plans if the stand is subjected to one or more tussock moth outbreaks.

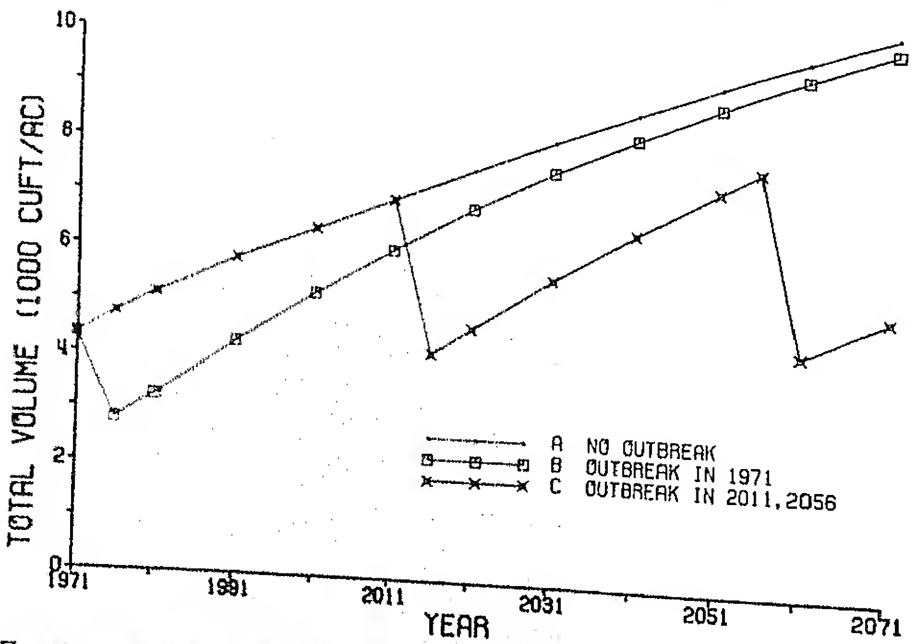

Figure 1.—An example of predicted total volume (ft³/acre) versus time for three Douglas-fir tussock moth (DFTM) outbreak scenarios: A, no outbreak; B, outbreak in 1971 only; C, multiple outbreaks in years 2011 and 2056.

Another advantage of such a simulation model is that the user can easily see the effect of varying most assumptions that have been made in describing stand and insect conditions. Those assumptions that are supported by the least reliable information can be examined in greater detail; an ad hoc sensitivity analysis can usually be performed rather easily and should point out the assumptions that are critical, as well as those that are not. If necessary, field sampling can then be used to increase the reliability of those assumptions that appear to be either critical or weak.

The Stand Prognosis Model

Stage (1973) described a Stand Prognosis Model that has become an increasingly useful tool in examining long-term stand management alternatives (Stage et al. 1980). The Stand Prognosis program is an individual tree-based stand model designed to simulate the development of the mixed-species even- and uneven-aged stands commonly found in the Northern Rocky Mountains. The simulator consists of separate component models for tree diameter growth, height growth, crown ratio, and mortality. The projection is produced by the repeated addition of periodic increments on diameter, height, and crown ratio to the initial dimensions of the inventoried trees. Numbers of trees are reduced by periodic mortality rates. Normal period length is 10 years.

Usual input for the Prognosis program is a list of tree and stand characteristics obtained from a standard stand inventory (Stage and Alley 1972). The diameter and species of each sample tree is required, while only a subsample of total height, crown ratio, and past growth is anticipated (but not required); spatial information describing individual tree locations is not used. Site characteristics sampled include slope, aspect, elevation, habitat type, and geographic location; measures of stand density are calculated internally from the list of tree characteristics. Information describing the sampling design is also required so that the number of trees per unit area represented by each sample tree can be calculated (Stage 1978d). Stand statistics, such as basal area or volume per unit area, are then calculated by summing the corresponding tree characteristics, weighted by the number of trees represented by each tree. Thus, the Prognosis Model can be used to display relevant stand statistics versus time even though the basic unit in the model is an individual tree. A more detailed discussion of the use of the Stand Prognosis Model in timber management applications is given by Stage (1978 et seq.) and Stage et al. (1980).

The Douglas-fir Tussock Moth (DFTM) Outbreak Model

The DFTM Outbreak Model (Overton and Colbert 1976 et seq.; Colbert et al. 1979, 1981 [see footnote 1]; Overton et al. 1981 [see footnote 2]) simulates the course of events during a tussock moth outbreak on a collection of 1000 in^2 midcrown sample branches (see Mason 1970). The outbreak is assumed to be 4 years in duration, with each year corresponding to a distinct phase in the outbreak (Mason and Luck 1978). The model was calibrated using data obtained during the last (1971–74) Blue Mountains outbreak in northeastern Oregon (see Mason 1976, 1978; Wickman 1978 et seq.; Beckwith 1978). The major processes considered are insect survival, growth, and feeding and the associated host defoliation; an annual redistribution of insects between sample branches is also considered. To run the DFTM Outbreak Model, the following information is needed: insect population density, biomass of the new foliage and either percentage new foliage or biomass of the old foliage; the foliage information is needed for each of the host species considered (Douglas-fir and grand fir). Colbert and Wong (1979) have detailed the procedures for running this simulation model independently of the Stand Prognosis Model; see Colbert et al. (1979) for further documentation. Additional discussion has been provided by Overton and Colbert (1978a, b,c) and Colbert (1978). The version of the DFTM Outbreak Model (version 3.1) used as subroutines in the Combined Model discussed in this paper is the same as that described by Colbert and Wong (1979) and Colbert et al. (1979), except that the output tables have been deleted.

The Combined Model

To properly use these two rather disparate models in conjunction, an understanding of the following topics is necessary:

1. Tree defoliation effects considered by the model,
2. Foliage biomass classification model,
3. Tree class compression,
4. Methods for allocating first instar larvae to tree classes,
5. Probability of outbreak model,
6. Outbreak control and salvage options available.

Each of these topics was discussed in detail by Monserud (1978a). A brief discussion will be given here.

Tree Defoliation Effects

A tussock moth outbreak can affect normal tree development in three major ways:

1. Growth in height and diameter can be retarded,
2. Total height and volume can be reduced because of top-kill, and
3. Probability of mortality can increase.

Although there may be other effects (for example, fertilization due to rapid nutrient turnover following defoliation), only these three are simulated in this model. The research basis for the quantification of these defoliation effects is due almost entirely to the work of B. E. Wickman, at the Corvallis Forestry Sciences Laboratory (for examples, see Wickman 1978a,b; Wickman et al. 1980).

Output from the DFTM Outbreak Model consists of percentage midcrown branch defoliation in Phase II and Phase III of the outbreak for each tree or class of similar trees. Maximum defoliation on the midcrown branch is then converted to percentage tree defoliation by the function described by Overton and Colbert (1978b), which is graphed in figure 2.

Two important characteristics of this function are:

1. Percentage of tree defoliation remains essentially zero until midcrown branch defoliation exceeds 55 percent;
2. Percentage of tree defoliation then increases rapidly until complete defoliation of both branch and tree is reached.

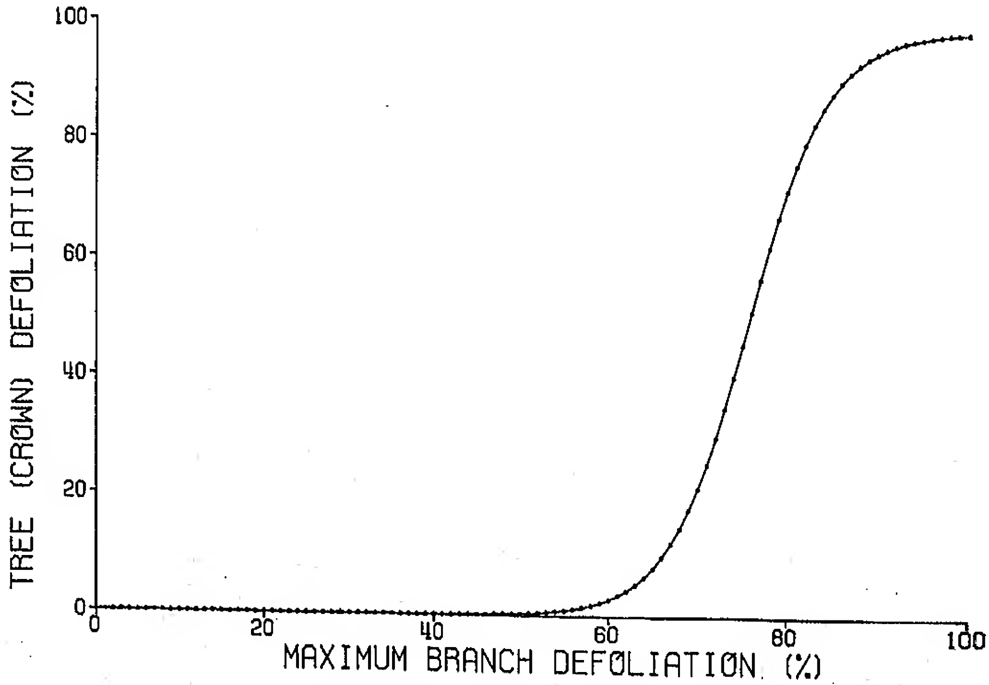

Figure 2.—Percentage tree crown defoliation versus percentage maximum midcrown sample branch defoliation (from Overton and Colbert 1978b).

It is very important to be aware of the behavior of this function when experimenting with the Combined Model, for a seemingly minor change in initial conditions could result in a dramatic change in tree defoliation if branch defoliation is between 70 and 90 percent. And any combination of control options or initial conditions that keep branch defoliation from exceeding 55 percent will produce results essentially identical to a simulation with no tussock moth outbreak at all.

Percentage of tree defoliation for a particular tree or class of similar trees is then used to index the table of defoliation effects (see Table 11-2 on p. 226 of Colbert and Campbell 1979, and discussion by Monserud 1978a, p. 65–66); note that the sampling basis for the defoliation effects is approximately 5 years (Wickman 1978a). This table contains the following species-specific information for seven tree defoliation classes:

1. Probability of direct mortality caused by tussock moth;
2. Probability of secondary and background mortality,
3. Probability of top-kill occurring on surviving trees for each of five top-kill classes;
4. Percentage of diameter and height growth reduction.

With the exception of calculating volume loss due to top-kill (Monserud 1980, 1981) the modification of tree characteristics resulting from defoliation is straightforward.

Foliage Biomass

The DFTM Outbreak Model of Overton and Colbert (1976) simulates the course of events during an outbreak on a collection of midcrown sample branches of 1000-in^2, as described by Mason (1970). The sample branch has only three essential characteristics: host species (Douglas-fir or grand fir), percentage new foliage, and total foliage biomass. Since the basic unit in the Stand Prognosis Model is a tree, and the basic unit in the Outbreak Model is a branch, a linkage between these units is needed to combine the two models. Species-specific equations for predicting foliage biomass characteristics of the sample branch, from tree and stand information available to the stand model, facilitate this linkage. Available equations were developed by C. R. Hatch at the University of Idaho (Hatch and Mika 1978; Monserud 1978a, p. 49–56). Unfortunately, the data base supporting these equations is quite limited, and should be improved. By sampling for the mean and standard deviation of the necessary foliage characteristics, the user is likely to increase the accuracy of the resulting simulations.

Tree Class Compression

The current version of the Stand Prognosis Model (Inland Empire version 4.0, as documented by Wykoff et al. 1982) can handle up to 1,350 individual tree records. Even when the number of records in a sample stand is small, the record tripling logic described by Stage (1973, p. 12–13) will usually result in several hundred tree records being projected. The DFTM Outbreak Model, however, only views trees in two dimensions (foliage biomass and percent new foliage) for each host species. Considerable computer time can therefore be saved by "compressing" trees with similar foliage biomass characteristics into the same tree class before the Outbreak Model is called (see discussion preceding the NUMCLASS keyword in a following section). Each "tree class" represents one or more tree records in the stand model and is represented by one midcrown sample branch (Mason 1970) in the Outbreak Model. The current version of the Combined Stand Prognosis and DFTM Outbreak Model allows for a maximum of 100 tree classes; this arbitrary limit appears to provide quite adequate resolution for simulating defoliation effects.

Allocation of First Instar Larvae

In addition to the foliage biomass information, the Tussock Moth Outbreak Model requires the specification of the number of established first instar larvae for each tree class at the start of an outbreak (Phase I). A tree class is simply a class or group of similar trees represented by a single midcrown sample branch. Note that "first instar larvae" in this paper should be considered synonymous with "viable eggs" in earlier papers (e.g., Monserud 1978a,b).

Two methods—assumptions, actually—are currently available for allocating levels of first instar larvae to the tree classes: the first is random and the second is deterministic. These methods allow for examining the various assumptions concerning the between-tree distribution of larvae in a stand.

With the random method, the number of larvae assigned to a particular tree class is drawn from a random normal distribution with specified mean and standard deviation. This option is quite useful when a sample of early instar larvae is available for a stand, assuming that no relationship can be found between larval density and observable tree characteristics. The random method also contains a feature that allows the user to vary the mean larval density if multiple outbreaks are being simulated.

The deterministic allocation method assigns three specified larval levels or densities to each ordered third of the tree classes, after the tree classes have been sorted by average diameter; the first tree class to have larvae assigned to it has the largest average diameter.

Wickman (1978a) reported on the distribution of mortality by diameter class in the last Blue Mountains outbreak. Either of these larval allocation assumptions could be used to mimic the evenly distributed pattern (with respect to diameter) of mortality for grand fir. The deterministic assumption, however, would be most amenable to reproducing the distribution of mortality reported for Douglas-fir, which was more concentrated in smaller diameter trees.

The actual levels of larvae specified with any of these options should be based on the most reliable estimates available, for this is the most important variable in the outbreak model. The choice of the assumption or method most appropriate for a particular situation should—if possible—be determined by analyzing tussock moth inventory data in relation to tree diameter or size. If this is not possible, we recommend using the random allocation method.

Probability of Outbreak

The DFTM Outbreak Model is just that—it simulates the course of events during a tussock moth outbreak. It was not designed to model population dynamics when the tussock moth is not at outbreak levels. Thus, the crucial decision of whether or not to invoke an outbreak must be made before the DFTM Outbreak Model is called. This forces consideration of the probability of an outbreak occurring in a given stand, in a given year.

The salient features of past outbreak patterns (Stage 1978a) are: outbreaks appear to be synchronized over large areas; intervals between outbreaks are usually at least 8 years; some stands are involved in repeated outbreaks, while others are involved only once; and not all the stands with similar conditions and histories are involved in a given outbreak.

These four features can be represented by the two-step process described by Stage (1978a). First, a sequence of dates is stochastically determined that represent the times when large-area outbreaks are to be simulated. This sequence represents the temporal probability of outbreak. Second, the relative probability with which a stand of particular attributes can be expected to show defoliation at the time specified by step one is then determined; this is the spatial probability of outbreak, conditional on the temporal probability of outbreak. The model used to predict the spatial probability of outbreak was developed by Heller et al. (1977), and uses both physiographic variables (slope, aspect, elevation, topographic position) and stand variables (crown closure, percent host species, average crown diameter). A similar outbreak model has recently been developed for the Palouse Ranger District (Clearwater National Forest) northeast of Moscow by P. B. Mika and J. Moore (personal communication 1979; see Stoszek et al. 1981 for a related analysis) at the University of Idaho. Mika and Moore's model was developed from data collected on ground plots, whereas data used by Heller et al. (1977) was obtained from aerial photographs in the Blue Mountains and Colville areas. The long-term accuracy of these models for predicting the conditional probability that a given stand will be involved in a regional outbreak is unfortunately unknown, for they are developed from data collected in only one regional outbreak (1971–74). Such models are also likely to be conditional on the specific (and unquantified) climatic factors associated with the 1971–74 outbreak.

The use of the probability-of-outbreak model is not a necessary feature of the combined system; an option is available for simulating any predetermined sequence of outbreaks. This option is quite useful for making retrospective comparisons of management alternatives when a stand's outbreak history is known.

Outbreak Control and Stand Management Options

The DFTM Outbreak Model can be used to simulate a number of control options—biological as well as chemical—by altering mortality rates at specific occasions in the outbreak. In the combined model, a simulated chemical control can be applied to any instar in any phase of the outbreak with any efficacy. Biological control options are available for applying nuclear polyhedrosis virus (NPV) in either Phase II or Phase III of the outbreak.

A wide variety of silvicultural options are also available in the Stand Prognosis Model. Thinning is simulated by reducing the number of trees per acre represented by the tree records until a user-specified thinning target is reached. The thinning target can be specified as:

a residual number of trees per acre;

a residual basal area per acre;

a segment of the diameter distribution;

a percentage of full stocking;

a prescription where specific tree records are coded for cutting.

The first three targets can be reached by thinning either from above or below. These thinning options can be implemented in any cycle of a simulation. Options are also available for specifying species preferences for harvesting that would allow for selectively removing host species. Use of the thinning options is discussed by Wykoff et al. (1982).

An additional harvesting option is also available in the Combined Model: a salvage thinning operation immediately following the outbreak can be requested. All host trees that have been defoliated more than a (user-supplied) minimum percentage tree defoliation will be salvaged. Thus some of the volume that normally would be lost due to tussock moth can be recovered. Of course, this will usually result in harvesting additional trees that are partially defoliated, but not killed—as happened in the last Blue Mountains outbreak.

DOCUMENTATION OF INPUT OPTIONS

The Combined Stand Prognosis/DFTM Outbreak Model utilizes a **keyword** system for specifying program options. The keywords are intended to simplify the process of specifying the various features of the model that will be implemented in a given simulation or run. The keyword system is analogous to a high level (albeit simple) computer language in which each instruction or keyword is translated into a number of complicated instructions. To invoke a particular option, the user simply inserts a short keyword in the runstream that is sent to the computer. For example, the keyword NPV2 specifies the application of nuclear polyhedrosis virus in Phase II (2) of an outbreak; although four separate tussock moth mortality rates need to be altered to simulate this option, these rates do not need to be provided by the user. The user is required to supply much less information to effect the desired result. Furthermore, the order that the information or keywords are submitted is usually not important; of course there are exceptions to this rule (for example, the DFTM keyword must precede all other tussock moth keywords). This keyword system is used extensively in the Combined Model, and has greatly simplified the process of preparing a simulation.

An additional simplifying feature of the keyword system is that default values exist for almost all keywords. Only keywords for nonstandard options need be specified, and the only numeric (parameter) values necessary on such keyword cards are those that differ from the default parameter values. In addition, all options and parameter values are reset to the default values after projecting a given stand in a multi-stand simulation.

Rules for coding keywords:

1. All keywords start in column 1 of the keyword card or record.
2. Numerical values (termed "parameters") needed to implement an option are contained in seven numeric "fields" that are each 10 columns wide, beginning in column 11. A decimal point should be punched for all numeric values that are not integers, and integer values should either be right-justified in the numeric field or followed by a decimal point. If a decimal point is provided, the actual location of the numeric value within the 10 column wide field is unimportant.
3. Blanks that are coded in the numeric fields are not treated as zeroes. If a blank field is found, the default value will be used. If zeroes are to be specified, they must be punched. Thus, only the numeric values that are different from the default parameter values need be specified (in the appropriate field, of course).
4. When two or more conflicting options are encountered, the last one specified will be used.
5. The first tussock moth keyword must be DFTM, and the last tussock moth keyword must be END.

This paper documents only those keywords used to implement the various features of the tussock moth portion of the Combined Stand Prognosis/DFTM Outbreak Model. Documentation for the keywords used by the Stand Prognosis Model is provided by Wykoff et al. (1982). Although these additional keywords are necessary to run the Combined Model, they are not listed here to avoid duplication with Wykoff et al. (1982).

Keywords will be grouped into the following five categories in the subsequent sections: program execution options, outbreak timing options, outbreak initial conditions options, tree class compression and redistribution options, and outbreak control options. Each section will contain a definition and short description of relevant keywords. Most sections will end with examples illustrating the use of keywords to simulate specific situations.

Program Execution Options

The keywords for controlling program execution options serve four general functions. The DFTM and END keywords signal the Stand Prognosis Model that tussock moth keywords will follow and have ended, respectively. NODFRUN and NOGFRUN can be used to exclude either Douglas-fir or grand fir as a host for tussock moth. DEBUG, DEBUTREE, PUNCH, REPORT, and DATELIST provide supplemental (and occasionally voluminous) output useful for examining the program's behavior in greater detail than that afforded by the usual output. And RANNSEED allows the user to choose a different random number sequence in any of the routines related to tussock moth. With this last option, a user can assess the magnitude of the variability associated with the stochastic components of the Combined Model. We anticipate that the only keywords in this section that most users will need to use are DFTM, END, and RANNSEED.

Keyword	**Keyword Description**
DFTM	Signal the Stand Prognosis Model that tussock moth keywords follow; use of this keyword is *mandatory.*
END	Signal the Combined Model that the preceding group of tussock moth keywords has ended. Any number of groups of tussock moth keywords can be used, provided each group begins with the DFTM keyword and ends with the END keyword. Use of this keyword is *mandatory.*
NODFRUN and NOGFRUN	These keywords inhibit the DFTM Outbreak Model from simulating the activity of tussock moth on Douglas-fir (NODFRUN) and/or grand fir (NOGFRUN).

DEBUG — A large amount of intermediate output detailing the operation of the Combined Model will be printed. This and the following option should rarely be needed by the normal user.

DEBUTREE — Long tables of intermediate values associated with individual tree records will be printed.

PUNCH — The input values and parameter arrays needed by the DFTM Outbreak Model as well as the defoliation levels by tree class, species average, and stand average are written in card image format to a separate output unit.

Field 1: The FORTRAN data set reference number where the supplemental output is written; there is no default.The user must specify a valid number and the corresponding job control statement.

REPORT — Control the amount of tussock moth output generated by the Combined Model; default is 2.

Field 1: The report level, where:
0 = no tussock moth output will be generated;
1 = only the DFTM Outbreak Summary Table will be printed;
2 = All normal tussock moth output tables will be printed (described in the INFORMATION PRODUCED section).

DATELIST — All tussock moth subprograms (i.e., subroutines and functions) and common blocks are listed with the date each was most recently revised.

RANNSEED — The pseudorandom number generator (Marsaglia and Bray 1968) used by the Combined Model has three seeds. These seeds initialize the random number generator, and are set at the beginning of each simulation. As a result, the random numbers will be generated in the same order each time a runstream is submitted. Consequently, identical projections of a single stand made in separate runstreams will have identical results. You can introduce some random variation by replacing one or more of the seeds. Since the new seeds should be odd integers, 1 will be added to any even numbers that are used to reseed the random number generator. Note that this random number generator is used only by the tussock moth related subroutines in the Combined Model; the Stand Prognosis Model has a separate, but identical, random number generator that is unaffected by this reseeding.

Field 1: First seed; the default is 1409859205.

Field 2: Second seed; the default is 402656419.

Field 3: Third seed; the default is −328609067.

Outbreak Timing Options

As discussed in the "Probability of Outbreak" section, specifying the time periods that the DFTM Outbreak Model is to be called is a two-step process. The first step schedules the occurrence of regional tussock moth outbreaks. This step can be handled in two different ways: manually (deterministically), using the MANSCHED keyword, or randomly, using the RANSCHED keyword. The second step selects which regional outbreaks will include the subject stand. The MANSTART keyword specifies that the subject stand will be included in all regional outbreaks; the RANSTART keyword makes this determination random, conditional upon the stand's probability of outbreak. The PROBMETH keyword specifies

the method for calculating the stand's conditional probability of outbreak. The TOPO and ASHDEPTH keywords provide information on topographic position and ash depth, required by some of the options available with the PROBMETH keyword.

MANSCHED — Manually specify either the calendar year or the cycle number in which a regional outbreak will occur; the default is for *NO* regional outbreaks to occur. If more than one regional outbreak is to be scheduled, use additional MANSCHED keywords.

Field 1: Either the year or the cycle number in which a regional outbreak will occur; default is for no regional outbreak to occur. NOTE: The Combined Model assumes that a number in Field 1 is a cycle number if it is less than or equal to 40—the maximum number of cycles (i.e., growth projection periods) allowed by the Stand Prognosis Model.

RANSCHED — Invoke the random automatic scheduling process which will stochastically generate a list of regional outbreaks which occur during the simulation period (see Stage 1978a). This is done by drawing from a random Bernoulli process with a specific minimum waiting time (Field 1) and a specific event probability (Field 2); the process begins with the year of the last regional outbreak (Field 3).

Field 1: The minimum waiting time between regional outbreaks; default is 30 years.

Field 2: The event probability used in the random Bernoulli process; default is 0.1. This is essentially the annual probability of a regional outbreak given that the minimum waiting time since the last outbreak has been exceeded. Note that the expected value of the time (T) between outbreaks is $T = M + (1/P) - 1$, where M is the minimum waiting time (Field 1) and P is the event probability (Field 2).

Field 3: The calendar year of the last regional outbreak; default is year 1492.

MANSTART — Specify that the DFTM Outbreak Model will be called whenever a regional outbreak is scheduled. MANSTART is the default "start" option.

RANSTART — Stochastically determine if the subject stand will be included in the regional outbreak. This is done by calculating a conditional probability (determined by the method specified in Field 1 of the PROBMETH keyword), that the subject stand will be infested by tussock moth, given that there is a regional outbreak. If this conditional probability is greater than a uniform random number between 0 and 1, then the regional outbreak includes the subject stand.

PROBMETH — Select a method for calculating the conditional probability that the subject stand will be included in a regional outbreak. This keyword is normally used in conjunction with the RANSTART keyword. If this keyword is used with the MANSTART keyword, the conditional probability of outbreak calculations will be made and printed in the "DFTM Outbreak Summary Table" (discussed in a later section), but will otherwise be ignored by the program.

Field 1: The conditional probability calculation method (default is method 1), where:

1 = Use the model developed by Heller et al. (1977), which is a

function of elevation, slope, aspect, topographic position, stand closure, proportion of stand in host, and average crown width. The last of these three variables are calculated as functions of crown competition factor. This model was calibrated using aerial photo interpretation data from the Blue Mountains of northeastern Oregon. See the TOPO keyword below for details concerning the topographic position specification.

2 = Use a model developed by Mika and Moore (personal communication, 1979) which is a function of topographic position (see TOPO), ash depth in inches (see ASHDEPTH), total basal area, and proportion of the stand in grand fir. This model was calibrated using data collected from the Palouse Ranger District of the Clearwater National Forest, northern Idaho.

3 = Use a model similar to 2 above, except that ash depth is not used. This model was developed using the same data used to develop model 2.

Field 2: The conditional probability scaling factor.[3] The default scaling factor is 1.0; a value of 0.5 would reduce the calculated conditional probability by half, and a value of 2.0 would double the calculated value.

TOPO

This keyword is used in conjunction with the PROBMETH keyword to enter the numeric code specifying the topographic position of the stand. When the conditional probability calculation method (Field 1 of the PROBMETH keyword) is 1, TOPO codes are:

1 = ridgetop
2 = sidehill
3 = bottom.

When the conditional probability calculation method is 2 or 3 (in Field 1 of the PROBMETH keyword), TOPO codes are:

1 = ridgetop or upper slope
2 = midslope or lower slope.

Field 1: Topographic position code (default is 1).

ASHDEPTH

When the conditional probability calculation method (specified in Field 1 of the PROBMETH keyword) is 2, the soil ash (loess) depth is needed to calculate the conditional probability that the subject stand will be involved in a regional outbreak.

Field 1: The ash depth in inches (default is 15.93).

The following two examples illustrate the use of several of the preceding keywords in tailoring a simulation to specific situations.

[3]Note that the available conditional probability of outbreak models were all developed using data describing stand conditions in only one regional outbreak—the 1971-74 outbreak. Such models predict conditional probability of outbreak only as a function of site and stand characteristics, even though the dependent variable is also conditional on a number of unobserved factors, such as climate and weather. The fact that such climatic factors are very difficult to quantify and relate to specific outbreak histories (Mason and Luck 1978) does not make the probability of stand outbreak models any less conditional on the specific climatic factors associated with (and perhaps peculiar to) the 1971-74 outbreak. The potential for such models to overestimate the probability of a stand being involved in future outbreaks is large, in our opinion.

Example 1.

You desire to simulate the following conditions. You hypothesize that the annual probability of a regional tussock moth outbreak occurring is 0.1, given that at least 20 years has elapsed since the last tussock moth outbreak (which occurred in 1971). You want to use Heller's model to stochastically determine whether or not there will actually be an outbreak in the sample stand if there is a regional outbreak. You believe, however, that Heller's model overestimates the conditional probability of stand outbreak by a factor of 4. Furthermore, you are curious to see just what the "large amount of intermediate output detailing the operation of the Combined Model" looks like. Finally, you would like to use the default values of all other keywords. The following group of tussock moth keywords will accomplish this:

```
DFTM
RANSCHED      20.      0.1      1971.
RANSTART
PROBMETH       1.      0.25
DEBUG
END
```

Example 2.

You would like to see how the results from the simulation described in example 1 are changed when you reseed the random number generator. You are also no longer curious to see the additional output DEBUG produces. Adding the RANNSEED keyword with any three odd numbers (and deleting DEBUG) will accomplish this:

```
DFTM
RANSCHED      20.      0.1      1971.
RANSTART
PROBMETH       1.      0.25
RANNSEED      13.      571.     14327.
END
```

Outbreak Initial Conditions

The DFTM Outbreak Model requires information describing tussock moth population levels and foliage biomass at the start of an outbreak (Phase I), on a 1000-in² midcrown sample branch basis. Recall that this sample branch represents a group or class of trees in the outbreak model. Larval density at the start of every outbreak can be assigned either randomly (RANLARVA) or deterministically (DETLARVA) for each host species; the same method must be used for both host species. The BIOMASS keyword specifies how foliage biomass is to be determined. And if sample-based estimates of the mean and standard deviation of the foliage distribution are available, they can be incorporated via the DFBIOMAS and GFBIOMAS keywords.

RANLARVA — Randomly allocate first instar larvae to the tree classes at the start of every outbreak. Note that this is the default larval allocation method. The host species is specified in Field 1; larval density is drawn from a normal distribution with mean specified in Field 2 and standard deviation specified in Field 3. The mean larval density (Field 2) may vary from outbreak to outbreak if the between-outbreak standard deviation (Field 4) is positive.

Field 1: Host species:
1 = Douglas-fir, and 2 = grand fir.

Field 2: The average number of first instar larvae per midcrown sample branch for the host species specified in Field 1; defaults are 9 and 11 larvae per sample branch for Douglas-fir and grand fir, respectively.

Field 3: The within-outbreak standard deviation of first instar larvae; default is 2.0 larvae for both host species.

Field 4: The between-outbreak standard deviation of first instar larvae; default is 0.0 for both host species. If this parameter is positive, the average larval density for the proper host species will be randomly chosen at the start of every outbreak by drawing from a normal distribution with mean specified in Field 2 and standard deviation specified in Field 4. Larvae will then be allocated to individual tree classes by randomly drawing from a normal distribution with this randomly chosen mean, and standard deviation specified in Field 3. This feature is best suited for use with the keywords that produce multiple outbreaks (primarily RANSCHED).

DETLARVA Deterministically assign different levels or densities of first instar larvae to each third of the tree classes, after sorting the tree classes by average diameter (in descending order).

Field 1: Host species:
1 = Douglas-fir, and 2 = grand fir.

Field 2: The number of larvae assigned to the largest third of the tree classes; defaults are 11 and 15 for Douglas-fir and grand fir, respectively.

Field 3: The number of larvae assigned to the middle third of the tree classes; defaults are 9 and 10 for Douglas-fir and grand fir, respectively.

Field 4: The number of larvae assigned to the smallest third of the tree classes; defaults are 7 and 5 for Douglas-fir and grand fir, respectively.

BIOMASS Specify the method for calculating foliage biomass (in grams) and percentage new foliage on the 1000-in^2 midcrown sample branches; default is method 4.

Field 1: The calculation methods are:

1 = The foliage biomass and percentage new foliage values will be randomly drawn from a normal distribution. The default mean and standard deviation of the foliage biomass distribution is 215g and 64g for Douglas-fir and 227g and 64g for grand fir, respectively (from Hatch and Mika 1978, p. 16). The default mean and standard deviation of the percentage new foliage distribution is 27 and 13 for Douglas-fir, and 35 and 7 for grand fir, respectively (from Hatch and Mika 1978, p. 21). These defaults can be replaced by using the DFBIOMAS and GFBIOMAS keywords.

2 = The species-specific equations developed by Hatch and Mika (1978) are used deterministically to predict the percentage new foliage and foliage biomass from tree and site variables. Because the equations behave poorly, Monserud (1978a) recommended that this option not be used.

3 = Species-specific equations developed by C. R. Hatch, University of Idaho (see Monserud 1978a, p. 55) will be used to deterministically predict percentage new foliage and foliage biomass; the only independent variable is basal area percentile.

4 = Same as method 3, but with a random normal error (with mean = 0) added to each prediction. The standard deviation of this random error distribution equals the standard error of the regression fit described in method 3. For foliage biomass, the standard deviation is 57g for Douglas-fir and 58g for grand fir; for percentage new foliage, the standard deviation is 11 for Douglas-fir and 7 for grand fir (see Monserud 1978a, p. 55).

DFBIOMAS — Used to replace the default parameter values determining Douglas-fir sample branch foliage biomass, when method 1 is specified on the BIOMASS keyword; foliage biomass and percentage new foliage will be randomly drawn from a normal distribution with mean and standard deviation specified by Fields 1 through 4:

Field 1: The mean of the foliage biomass distribution for Douglas-fir; default is 214g.

Field 2: The standard deviation of the foliage biomass distribution for Douglas-fir; default is 64g.

Field 3: The mean of the percentage new foliage distribution for Douglas-fir; default is 27.

Field 4: The standard deviation of the percentage new foliage distribution for Douglas-fir; default is 13.

GFBIOMAS — Same as DFBIOMAS, but for grand fir; used in conjunction with BIOMASS method 1.

Field 1: The mean of the foliage biomass distribution for grand fir; default is 227g.

Field 2: The standard deviation of the foliage biomass distribution for grand fir; default is 64g.

Field 3: The mean of the percentage new foliage distribution for grand fir; default is 35.

Field 4: The standard deviation of the percentage new foliage distribution for grand fir; default is 07.

Example 3.

You would like to make a projection with only one DFTM outbreak. You also want this outbreak simulated in year 1971 (which happens to be when the first cycle of the projection begins). You have estimated that the outbreak probably began in this stand with an average of nine first instar larvae per 1000-in² midcrown sample branch on Douglas-fir, and 12 larvae per sample branch on grand fir; your best estimate of the standard deviation is approximately four larvae per sample branch on either host species. You prefer to use biomass method 1 rather than the default method (4). The following keywords will accomplish this (note that MANSTART is supplied by default):

```
DFTM
MANSCHED     1.
RANLARVA     1.     9.     4.
RANLARVA     2.    12.     4.
BIOMASS      1.
END
```

Example 4.

You want to modify the simulation in example 3 to include multiple outbreaks that are stochastically determined but occur approximately every 45 years, with a minimum waiting time of 36 years (note that these assumptions imply an annual probability of regional outbreak of 0.1). You have very little information on how outbreak severity varies in the long run, but you are sure that it is not constant; thus you assume that the between-outbreak standard deviation of larval density is approximately 5 larvae for both host species. You would also like to modify your foliage biomass assumptions as follows: Mean foliage biomass of a 1000-in² midcrown sample branch is 100g and 200g for Douglas-fir and grand fir, respectively, while mean percentage new foliage is 20 percent for Douglas-fir and 30 percent for grand fir; you have no information that warrants replacing the default foliage standard deviations. The following keywords will mimic these assumptions:

```
DFTM
RANSTART
RANSCHED      36.     0.1    1971.
RANLARVA       1.     9.       4.     5.
RANLARVA       2.    12.       4.     5.
BIOMASS        1.
DFBIOMAS     100.             20.
GFBIOMAS     200.             30.
END
```

Tree Class Compression and Redistribution Options

Before the DFTM Outbreak Model is called, the list of up to 1,350 tree records carried by the Stand Prognosis Model is compressed into a maximum of 100 groups or classes of trees (see NUMCLASS and WEIGHT). The purpose of this compression is to save computer time, by combining trees that are similar (as far as the DFTM Outbreak Model is concerned) into the same tree class. Once these tree classes have been created, the rate at which insects are assumed to annually redistribute between tree classes can also be specified (see REDIST). It is anticipated that very few users will have need of the keywords discussed in this section (viz., NUMCLASS, WEIGHT, REDIST). The default values should be adequate for most applications.

As previously mentioned, only two tree characteristics (for a given species) are important to the DFTM Outbreak Model: the percentage new foliage and foliage biomass of the midcrown sample branch. Recall that these two foliage attributes are assigned to each tree using the procedures described with the BIOMASS keyword. The compression routine is simply a procedure for deciding which trees are most alike with respect to their foliage complements.

Two keywords control this compression: NUMCLASS and WEIGHT. The relative importance of the two foliage characteristics is determined by WEIGHT. And the NUMCLASS keyword determines the number of tree classes (Field 1 or 2, depending on the species) to be created, using the following procedure:

1. The mean and standard deviation for each foliage characteristic are calculated. Each tree's foliage characteristics are then "standardized" by subtracting the mean and dividing by the standard deviation of the appropriate foliage characteristic.

2. A new attribute is then created for each tree; call this attribute A. This attribute is the weighted sum of the standardized foliage characteristics; the weights used to multiply each standardized foliage characteristic in this sum are specified on the WEIGHT keyword card. Attribute A is then sorted into descending order, and used by the following two compression algorithms to assign trees to tree classes:

3. The first compression algorithm finds the largest gaps (or differences or distances) between adjacent sorted A values. These gaps become the boundaries for compression. All trees between two adjacent gaps are classified or grouped into the same tree class. This algorithm is intended to find those trees (or groups of trees) that have foliage characteristics that are very unusual, and should therefore not be combined with other trees into the same tree class. Generally speaking, this first compression algorithm does a good job of finding

such unusual trees, but in the process creates a few tree classes that contain a large number of trees (which are relatively similar). Additional discussion of this algorithm is given by Monserud (1978a, p. 59-61; see rule 4B). The proportion of the total number of tree classes determined by this algorithm is specified by parameter 3 of the NUMCLASS keyword.

4. The remaining available tree classes are determined by the second compression algorithm, which works as follows: The tree class containing the largest number of tree records is split into two classes, so that each class contains half of the records in the original class. Again the tree class containing the largest number of tree records is found, and then split evenly into two classes. This algorithm is repeated until the number of tree classes specified on the NUMCLASS keyword is created. The second compression alogrithm is intended to insure that one tree class does not contain an excessively large number of tree records, even though the foliage characteristics of those trees are relatively similar.

NUMCLASS — Specifies the number of tree classes to be created for each host species (Fields 1 and 2), and the proportion of tree classes to be created by the first tree compression algorithm (Field 3). All trees in a given tree class will be represented by one midcrown sample branch in the DFTM Outbreak Model.

Field 1: Number of Douglas-fir tree classes; default is 20.

Field 2: Number of grand fir tree classes; default is 20. (Note: the sum of Fields 1 and 2 must not exceed 100)

Field 3: Proportion of tree classes determined by the first tree class compression algorithm (see preceding discussion); default is 0.50.

WEIGHT — Specify the relative importance of the two foliage variables used by the algorithm for compressing the list of trees into the number of tree classes specified by the NUMCLASS keyword (see discussion preceding NUMCLASS keyword). The default values result in percentage new foliage and foliage biomass being equally important.

Field 1: The weight given to percentage new foliage; the default value is 1.0.

Field 2: The weight given to foliage biomass; the default value is 1.0.

REDIST — Specify the annual redistribution rate of insects between tree classes (see Colbert and Wong 1979, p. 54). In effect, the redistribution rate (Field 1) operates by reducing the variation between the number of insects per tree class (weighted by the number of trees per tree class). The default redistribution rate of 0.25 will reduce the between tree class variation in insects by 25 percent for each year of the outbreak. A rate of 0.0 results in no redistribution, and a rate of 1.0 results in completely uniform redistribution, with the same number of insects in each tree class after the first year of the outbreak.

Field 1: The annual tussock moth redistribution rate; default is 0.25.

DFTM Control and Stand Management Options

The CHEMICAL, NPV2, and NPV3 keywords are available for simulating the effect of applying either a chemical control or a virus, at various occasions during the outbreak. If the user desires to simulate a control measure that is not in the available list, then the TMPARMS keyword can be used to alter the appropriate mortality rates or growth parameters in the DFTM Outbreak Model; in this case, Colbert and Wong (1979) must be consulted to calculate the appropriate parameter value. A SALVAGE option is also available.

CHEMICAL — Chemical control will be applied in the phase of the outbreak specified in Field 1 to the instar specified in Field 2, and with the efficacy specified in Field 3. Note that any number of CHEMICAL keywords can be used.

Field 1: Phase (year) of the outbreak when chemical control will be applied; default is 3.

Field 2: Instar that will be targeted for control; default is 4.

Field 3: Instar specific mortality rate resulting from the chemical control treatment; default is 0.95.

NPV2 — Nuclear polyhedrosis virus will be applied in Phase II.

NPV3 — Nuclear polyhedrosis virus will be applied in Phase III.

SALVAGE — At the end of a tussock moth outbreak, salvage all surviving host trees that have been defoliated more than the percentage tree defoliation specified in Field 1.

Field 1: The minimum percentage tree defoliation for trees that will be salvaged; default is 50.0.

TMPARMS — This keyword has been provided for experienced users who have need to change additional parameters in the DFTM Outbreak Model. The parameters in question are most of those which make up the "PARAMETER" file as described in appendix A of Colbert and Wong (1979). The DFTM submodel described here contains an internal storage area which acts as a surrogate to their PARAMETER file; the TMPARMS keyword can be used to replace any parameter in this storage area. Colbert and Wong (1979) have defined the PARAMETERS and illustrated how new values are calculated. They have also prepared a table (see appendix A of their paper) which refers to the variables by data-card number, represented by the letter *i*, and value-on-the-card number, represented by the letter *j*. These same values, *i* and *j*, are used to reference the parameter values to be redefined in the Combined Model. Note that the parameter value will be reset to its default value if additional stands are processed in the same run.

Field 1: The card or record number (*i*, as described by Colbert and Wong 1979, p. 41–46), which contains the parameter to be replaced in the DFTM submodel storage area. The value of *i* must equal an integer from 2 to 12 or 19 to 25.

Field 2: The *j*th value on the *i*th card which corresponds to the parameter to be replaced in the DFTM submodel storage area. The value of *j* must equal an integer from 1 to 6.

Field 3: The value which is to replace the parameter corresponding to the *j*th value on the *i*th card in the parameter file. An error will occur if this or either of the preceding two fields are left blank.

To illustrate the use of the TMPARMS keyword, table 1 lists the parameter values for TMPARMS keywords that will mimic the two virus control keywords defined previously. When a virus control keyword (NPV2 or NPV3) is used, the instar-specific daily disease mortality rates listed by Colbert and Wong (1979, p. 42–43) are replaced by the mortality rates found in Field 3 in table 1.

Table 1.—Parameter values on the TMPARMS keyword(s) that will mimic the virus control keywords; note that four TMPARMS keywords are needed to mimic each of the virus control keywords

Keyword to be mimicked	Parameters of the TMPARMS keyword		
	Field 1	Field 2	Field 3
NPV2	3	3	0.036
	3	4	.039
	3	5	.042
	3	6	.072
NPV3	4	3	.036
	4	4	.039
	4	5	.042
	4	6	.072

Example 5.

You would like to rerun the simulation in example 3, but with the following additions: simulate a chemical control with 90 percent efficacy applied in Phase III of the outbreak to the second instar, and salvage all trees that were defoliated more than 75 percent:

```
DFTM
MANSCHED     1.
RANLARVA     1.      9.      4.
RANLARVA     2.     12.      4.
BIOMASS      1.
CHEMICAL     3.      2.      0.90
SALVAGE     75.
END
```

INFORMATION PRODUCED

The Combined Model displays a variety of output tables which summarize the operation of the DFTM Outbreak Model during the course of the simulation. The DFTM Options and Input Table summarizes and describes the keywords that are in effect during the simulation. The DFTM Outbreak Summary Table lists the information germane to the scheduling and timing of outbreaks. The DFTM Defoliation Statistics Table—which is produced for each outbreak—displays the effect of tussock moth defoliation on each tree class.

These tussock moth outputs supplement the normal output tables produced by the Stand Prognosis Model (see Stage 1973, and Wykoff et al. 1982 for examples). An example of each type of output will be provided in the following discussion. A listing of the runstream that produced the simulation output illustrated in this section can be found in appendix A.

DFTM Options and Input Table

A brief summary of the important tussock moth keywords and parameter values used in a given stand projection is contained in the DFTM Options and Input Table (fig. 3). The keywords are listed in the left-hand column. A short description of the keyword and the numeric parameter values used in the simulation then follow to the right, com-

```
DOUGLAS-FIR TUSSOCK MOTH IN DOUGLAS-FIR AND GRAND FIR:  DFTM VERSION 3.1;  PROGNOSIS (INLAND EMPIRE) 4.0

                              STAND ID= YRID-123; MANAGEMENT ID= F3T7

------------------------------------------- DFTM OPTIONS AND INPUT TABLE -------------------------------------------

KEYWORD    KEYWORD DISCRIPTION AND PARAMETER VALUES USED
--------   ---------------------------------------------------------------------------------------------------------

RANSCHED   REGIONAL OUTBREAKS AUTOMATICALLY SCHEDULED.
           MINIMUM WAITING PERIOD IS   30 YEARS; EVENT PROBABILITY IS  0.100
           LAST RECORDED TUSSOCK MOTH OUTBREAK WAS IN YEAR:  1492

RANSTART   STAND INCLUSION IN REGIONAL OUTBREAKS IS STOCHASTICALLY DETERMINED (SEE PROBMETH).

PROBMETH   CONDITIONAL PROBABILITY OF STAND BEING INCLUDED IN A REGIONAL OUBREAK IS A FUNCTION OF:
           ELEV, SLOPE, ASPECT, TOPO, CROWN CLOSURE, CROWN WIDTH, AND %HOST (METHOD 1)
           PROBABILITY SCALING FACTOR = 1.000

TOPO       TOPOGRAPHIC POSITION CODE =    1.00;  1=RIDGETOP,2=SIDEHILL,3=BOTTOM.

ASHDEPTH   SOIL ASH DEPTH IN INCHES =    15.930

RANLARVA   RANDOM FIRST INSTAR LARVAE ASSIGNMENT FOR SPECIES  1 (DF)
           AVERAGE =  14.00; WITHIN-OUTBREAK STANDARD DEVIATION =  2.00; BETWEEN-OUTBREAK STANDARD DEVIATION =  0.0

RANLARVA   RANDOM FIRST INSTAR LARVAE ASSIGNMENT FOR SPECIES  2 (GF)
           AVERAGE =  14.00; WITHIN-OUTBREAK STANDARD DEVIATION =  2.00; BETWEEN-OUTBREAK STANDARD DEVIATION =  0.0

BIOMASS    ASSIGNMENT USING BASAL AREA PERCENTILE AND SPECIES, WITH ADDITIVE RANDOM VARIATION (METHOD 4)

NUMCLASS   NUMBER OF REQUESTED CLASSES OF DOUGLAS-FIR=  20; GRAND FIR= 20
           PROPORTION OF CLASSES DEFINED BY FINDING DIFFERENCES BETWEEN TREES =  0.50
           THE REMAINING CLASSES ARE FOUND BY HALVING THE CLASSES WITH THE MOST TREE RECORDS.

WEIGHT     THE CLASSIFICATION WEIGHTING FACTORS ARE:   1.00 FOR % NEW FOLIAGE, AND   1.00 FOR FOLIAGE BIOMASS.

REDIST     ANNUAL TUSSOCK MOTH REDISTRIBUTION RATE =  0.25

SALVAGE    SALVAGE SURVIVORS AFTER EVERY OUTBREAK.  CRITICAL TREE DEFOLITION LEVEL =  90.0%

RANNSEED   DFTM RANDOM NUMBER GENERATOR WAS RESEEDED:          49          69          89
--------------------------------------------------------------------------------------------------------------------
```

Figure 3.—Sample output from the Combined Model: DFTM Options and Input Table.

prising the main body of the table. Note that the DFTM Options and Input Table is designed to display only the options in effect for the simulation; it does not include all of the available keywords. Also note that the DFTM keywords that are explicitly specified by the user are also listed (in the order specified) in the "Options Selected by Input" table in the Stand Prognosis Model (see Wykoff et al. 1982 for an example).

DFTM Outbreak Summary Table

The DFTM Outbreak Summary Table (fig. 4) displays the timing of tussock moth outbreaks in summary form. The Combined Model contains logic that controls the process of selecting which cycles (i.e., projection periods) will contain a tussock moth outbreak. As discussed earlier, there are two steps in this decision process. The first step schedules the timing of regional outbreaks and the second determines which of the regional outbreaks will include the subject stand.

DFTM OUTBREAK SUMMARY TABLE

CYCLE NUMBER	CYCLE YEARS	YEAR OF REGIONAL DFTM OUTBREAK	CONDITIONAL PROBABILITY OF STAND OUTBREAK	WAS THERE AN OUTBREAK IN STAND YRID-123?
1	1971 - 1976	1971	0.843	YES
2	1976 - 1981		0.496	NO
3	1981 - 1991		0.542	NO
4	1991 - 2001		0.664	NO
5	2001 - 2006		0.740	NO
6	2006 - 2011	2006	0.763	YES
7	2011 - 2021		0.418	NO

Figure 4.—Sample output from the Combined Model: DFTM Outbreak Summary Table.

The first three columns of the Tussock Moth Outbreak Summary Table (fig. 4) list the outcome of the first step of the outbreak scheduling logic. A list of the Prognosis Model cycles is contained in the first two columns. The third column contains a list of the regional outbreak years. When the RANSCHED option is used, as is the case in this example, a series of regional outbreak dates are stochastically generated. These outbreak dates are assigned to existing projection cycles if one can be found that starts within ±2 years of the regional outbreak; otherwise a 5-year cycle is inserted.

The remainder of the table summarizes the second step of the outbreak decision logic. The fourth column contains a list of conditional probabilities that the subject stand will be included in the regional outbreak. Note that a conditional probability is printed for every cycle, even though there may be no regional outbreak scheduled in that cycle. In addition, note that these conditional probabilities are used only when the RANSTART option is specified (as it was in the example presented here). The last column indicates whether or not the subject stand was included in the regional outbreak; only then is the DFTM Outbreak Model called.

The user should be aware that the sampling basis of the DFTM damage model is approximately 5 years (Wickman 1978a). When the user specifies that cycle lengths other than 5 years are to be used, the Combined Stand Prognosis/DFTM Outbreak Model automatically inserts and/or deletes cycles such that each cycle which contains a tussock moth outbreak is 5 years long.[4] In the example simulation summarized in figure 4, 5-year tussock moth cycles were inserted in the first and next-to-last projection cycles; both cycles would have been 10 years long (1971–1981 and 2001–2011) in the absence of regional tussock moth outbreaks.

The insertion and/or deletion of cycles is done only when necessary. The timing of the Prognosis Model management options, such as thinning, will remain intact regardless of the number of cycles inserted. Occasionally the deletion of a cycle will force a management option to be rescheduled to the next available cycle. Warning messages are printed to inform of the action taken by the combined model.

eption to this rule. When MANSCHED scheduling is used in conjunction with the MAN- possible to force the Combined Model to simulate a 4- or 6-year long tussock moth outbreak. nese cases arises, a warning message will be printed.

DFTM Defoliation Statistics Table

Figure 5 illustrates the output summarizing each tussock moth outbreak. The first sever[al] lines contain a message indicating which years of the subject stand's development include the outbreak that is detailed in the rest of the table. A message is also printed indicating when a salvage is scheduled.

The main body of figure 5 consists of the "Summary of Tree Class Characteristics." A row of summary statistics is printed for each tree class, which is a collection of trees with similar foliage attributes—the only tree characteristics important to the DFTM Outbreak Model. These statistics are divided into two groups: "Before Outbreak" (columns 1-10) and "After Outbreak" (columns 11-19). The last three rows contain weighted averages of the same characteristics for each host species (Douglas-fir and grand fir) and for all host species combined. Except for the columns labeled "Records per tree class" and "Trees pe[r] acre" (columns 3 and 4), all summary statistics printed in this figure are averages weighted by the number of trees per acre (column 4) represented by each tree in a given tree class.

Percentage branch defoliation (column 11) is the only variable in figure 5 directly predicted by the DFTM Outbreak Model. Percentage branch defoliation is converted to percentage tree defoliation (column 12) using the function illustrated in figure 2. The insensitiv[ity] of percentage tree defoliation to any amount of branch defoliation below 55 percent ca[n] be seen from examining columns 11 and 12 in the "Summary of Tree Class Characteristics" table illustrated in figure 5; the extreme sensitivity of the relationship graphed in figure 2 is also apparent for values of branch defoliation between 60 and 90 percent. The predictions of mortality, top-kill, and diameter and height growth loss are all functions of percentage tree defoliation.

Recall that tree mortality (or survival) is modeled as a continuous rather than a discrete event in the Stand Prognosis Model (Stage 1973; Monserud 1978a). Mortality operates by reducing the number of trees per acre represented by a given tree record. Thus the number of trees per acre in a given tree class after the outbreak equals the product of the trees per acre before the outbreak (column 4) and 1.0 minus the 5-year mortality rate (column 13). Of course it would not be correct to attribute the reduction in trees per acre solely to the tussock moth, for the normal mortality rate in the absence of a tussock moth outbreak is certainly greater than zero.

Top-kill is not modeled in the same manner as mortality however, for top-kill is treated a[s] a discrete event in the combined model. Monserud (1978a, p. 67-68) detailed the procedure for stochastically determining whether or not a given tree will have top-kill, and how much. The average amount of top-kill for each tree class is summarized in columns 18 and 19 of figure 5. As a result of top-kill, the total height, live crown ratio, and volume of a tree are reduced accordingly; the procedure for calculating the volume of a top-killed tree is discussed by Monserud (1980, 1981).

The effect of tussock moth defoliation on diameter and height growth can be seen in columns 14-17 of figure 5; the sum of net growth and growth loss equals the growth in the absence of tussock moth defoliation. Note that the change in height columns (16 and 17) include top-kill losses. Because top-kill losses can potentially exceed height growth, net change in height can be negative (see column 16 in figure 5 for tree classes 9 and 22). The average amount of top-kill as a percentage of live crown length is displayed in column 19 of figure 5.

DFTM DEFOLIATION STATISTICS FOR STAND YRID-123; MANAGEMENT ID= F3T7

THE FIRST YEAR OF THIS SIMULATED TUSSOCK MOTH OUTBREAK IS YEAR 1971. IT IS BEING SIMULATED AS PART OF CYCLE 1 WHICH REPRESENTS YEARS 1971 TO 1976 IN THIS STANDS DEVELOPMENT.

SUMMARY OF TREE CLASS CHARACTERISTICS

		BEFORE OUTBREAK										AFTER OUTBREAK						
							MIDCROWN SAMPLE BRANCH			PRECENTAGE DEFOLIATION			5 YEAR CHANGE IN: DIAMETER		HEIGHT		AMOUNT OF TOP-KILL	
TREE CLASS NO.	HOST SPP.	RECORDS PER TREE CLASS	TREES PER ACRE	DBH (IN)	HEIGHT (FT)	LIVE CROWN RATIO	PERCENT NEW FOLIAGE	FOLIAGE BIOMASS (GRAMS)	FIRST INSTAR LARVAE	BRANCH (%)	TREE (%)	FIVE YEAR MORT RATE	NET (IN)	LOSS (IN)	NET (FT)	LOSS (FT)	(FT)	(%)
1	DF	1	0.4	24.9	85.1	0.48	37.4	400.0	14.2	91.25	95.39	0.591	0.05	0.07	1.13	0.25	0.0	0.0
2	DF	2	1.9	12.9	68.1	0.36	42.0	301.7	19.2	100.00	100.00	0.940	0.09	0.14	2.01	0.50	0.0	0.0
3	DF	5	5.8	18.7	88.6	0.48	41.7	263.3	14.5	100.00	100.00	0.940	0.14	0.23	1.89	0.47	0.0	0.0
4	DF	4	4.0	18.3	74.5	0.31	39.3	254.3	17.0	100.00	100.00	0.940	0.10	0.16	1.74	0.43	0.0	0.0
5	DF	2	3.0	9.4	52.3	0.47	25.5	317.1	14.8	100.00	100.00	0.940	0.11	0.18	2.68	0.67	0.0	0.0
6	DF	11	9.6	7.7	45.4	0.35	35.6	228.6	16.1	100.00	100.00	0.940	0.11	0.17	2.76	0.69	0.0	0.0
7	DF	6	4.4	10.6	63.1	0.34	31.1	241.3	14.7	92.75	96.18	0.591	0.15	0.24	2.76	0.73	0.2	1.3
8	DF	6	3.9	9.3	50.1	0.42	37.2	192.2	14.5	98.37	97.62	0.591	0.13	0.20	2.31	0.57	0.0	0.0
9	DF	7	4.7	9.0	51.1	0.41	28.8	224.4	14.5	84.34	86.16	0.373	0.23	0.17	-0.32	4.00	3.5	11.1
10	DF	7	5.6	6.5	41.9	0.40	26.5	225.1	12.1	88.45	93.06	0.373	0.18	0.14	0.97	2.50	2.1	11.2
11	DF	9	6.6	3.8	29.5	0.33	27.3	196.4	10.4	74.91	45.16	0.085	0.19	0.10	3.09	0.59	0.0	0.0
12	DF	11	8.5	7.4	43.2	0.37	20.0	213.8	12.9	69.42	19.45	0.076	0.23	0.09	2.70	0.67	0.4	2.0
13	DF	12	12.0	4.0	28.4	0.32	18.0	210.2	12.0	67.21	12.80	0.076	0.21	0.04	2.98	0.49	0.0	0.0
14	DF	11	9.4	3.1	22.7	0.21	24.9	155.0	16.2	95.66	97.14	0.591	0.08	0.13	2.58	0.53	0.0	0.5
15	DF	12	9.7	3.4	24.9	0.23	19.0	175.5	15.6	78.37	63.87	0.085	0.13	0.07	2.74	0.63	0.3	3.6
16	DF	11	6.2	3.4	25.2	0.30	19.5	156.4	12.2	77.75	60.70	0.085	0.17	0.09	2.76	0.51	0.2	2.8
17	DF	12	10.9	3.1	21.8	0.32	15.2	166.9	14.7	71.03	25.74	0.076	0.17	0.07	2.89	0.45	0.0	0.6
18	DF	11	8.5	3.0	22.6	0.29	14.8	142.4	12.9	70.60	23.91	0.076	0.18	0.07	2.89	0.51	0.0	0.3
19	DF	12	9.7	4.1	29.7	0.27	13.4	126.1	17.1	48.35	0.21	0.073	0.19	0.03	3.06	0.33	0.0	0.0
20	DF	7	7.6	1.7	12.4	0.21	11.2	93.3	12.7	28.36	0.00	0.070	0.17	0.03	2.45	0.15	0.0	0.0
21	GF	1	0.4	12.9	63.2	0.47	47.0	351.8	15.2	100.00	99.56	0.934	0.13	0.15	2.46	0.62	0.0	0.0
22	GF	2	2.1	11.8	59.2	0.46	39.5	374.1	14.5	86.82	90.94	0.266	0.43	0.34	-9.22	13.92	13.6	54.1
23	GF	2	1.0	15.4	64.8	0.58	47.0	303.6	11.5	99.29	97.72	0.555	0.48	0.58	3.93	0.97	0.0	0.0
24	GF	4	3.7	6.5	38.7	0.35	45.5	299.3	12.7	100.00	98.67	0.555	0.19	0.22	2.79	0.70	0.0	0.0
25	GF	3	3.6	7.2	34.2	0.29	43.5	304.2	9.2	92.16	95.90	0.555	0.23	0.28	2.51	1.32	0.8	32.0
26	GF	32	27.7	8.9	45.6	0.41	40.3	279.1	9.5	90.68	95.02	0.555	0.26	0.32	2.27	1.62	1.0	5.8
27	GF	32	27.0	8.4	47.4	0.38	39.5	254.7	13.2	100.00	100.00	0.934	0.23	0.28	3.07	0.77	0.0	0.0
28	GF	64	55.6	5.1	29.7	0.37	38.1	237.5	15.2	100.00	100.00	0.934	0.24	0.28	2.61	0.69	0.0	0.1
29	GF	32	29.1	4.9	29.0	0.34	37.7	213.1	16.1	97.05	97.42	0.555	0.21	0.26	2.33	0.82	0.3	3.1
30	GF	32	25.7	4.8	28.8	0.40	37.2	203.0	15.5	86.62	90.64	0.266	0.29	0.23	1.12	2.03	1.6	12.5
31	GF	64	49.9	5.2	30.3	0.34	33.9	206.6	16.4	87.96	92.50	0.266	0.30	0.24	2.48	0.89	0.4	4.6
32	GF	32	29.7	4.4	27.7	0.35	35.1	178.3	15.3	92.37	96.00	0.555	0.21	0.26	1.93	1.30	0.7	2.8
33	GF	32	23.1	5.1	28.6	0.31	33.1	181.2	10.8	86.83	90.96	0.266	0.28	0.22	2.65	0.50	0.0	1.0
34	GF	64	49.1	4.8	28.7	0.36	31.2	175.9	10.4	85.80	89.24	0.266	0.29	0.23	1.94	1.26	0.8	5.9
35	GF	64	57.4	3.6	22.0	0.32	29.6	154.5	14.4	89.70	94.27	0.266	0.26	0.20	2.18	0.70	0.3	4.1
36	GF	64	52.6	4.0	25.0	0.33	24.0	146.4	12.9	77.55	59.65	0.065	0.28	0.17	2.37	0.62	0.2	1.8
37	GF	1	0.4	1.8	10.2	0.28	21.3	125.0	14.5	74.26	41.63	0.066	0.10	0.06	1.67	0.42	0.0	0.0
38	GF	4	2.9	4.8	30.2	0.32	16.4	149.0	16.7	61.58	3.96	0.065	0.35	0.10	2.85	0.40	0.0	0.0
39	GF	1	0.6	1.8	10.2	0.32	17.5	125.0	14.9	65.01	8.21	0.066	0.54	0.15	1.81	0.27	0.0	0.0
40	GF	1	0.6	7.9	46.7	0.17	16.7	125.0	17.2	65.60	9.26	0.063	0.58	0.16	3.98	0.60	0.0	0.0
AVERAGE	DF	7.9	6.6	6.1	36.5	0.32	23.3	190.8	14.2	77.32	54.40	0.328	0.16	0.11	2.52	0.72	0.3	1.6
AVERAGE	GF	26.5	22.1	5.2	30.2	0.35	33.7	199.7	13.7	89.81	89.63	0.427	0.26	0.24	2.24	1.02	0.5	4.0
AVERAGE	HOST	17.3	14.4	5.4	31.7	0.35	31.3	197.6	13.9	86.93	81.51	0.404	0.24	0.21	2.31	0.95	0.4	3.4

Figure 5.—Sample output from the Combined Model: DFTM Defoliation Statistics Table.

ther Output

As discussed earlier, the defoliation estimates made by the DFTM submodel are automatically transmitted to the Prognosis Model and translated into tree damage. Thus, any tree mortality, growth reductions, and volume losses attributable to tussock moth are reflected in the normal output produced by the Stand Prognosis Model.

Figures 6 and 7 are examples of the two major displays produced by the Prognosis Mo these output tables are discussed by Stage (1973, p. 3–5) and Wykoff et al. (1982). An exa ination of figure 6 reveals that mortality losses were estimated to be 400 ft^3/acre/yr durin the simulated outbreak that began in 1971. During this outbreak, 52 percent of the volum lost was grand fir and 45 percent was Douglas-fir (see the species composition summary o the right half of figure 6). The outbreak was followed by a salvage that removed 989 ft^3/a in the year 1976 (all trees with tree defoliation exceeding 90 percent were salvaged). In fig 7 it can be seen that stand basal area was reduced from 173 ft^2/acre before the 1971 outbreak to 99 ft^2/acre after the outbreak; the salvage cut reduced it further to 57 ft^2/acre. I evident from both figures 6 and 7 that the combined model predicted that the stand contained 618 trees per acre before the 1971 outbreak, 382 trees per acre after the outbreak, a 210 trees per acre after the salvage at the end of the 1971 outbreak.

Finally, optional tussock moth output is printed if the user specifies the proper keyword(s); see the descriptions of the DEBUG, DEBUTREE, and PUNCH keywords for details.

STAND GROWTH PROGNOSIS SYSTEM VERSION 4.0 -- INLAND EMPIRE

STAND ID: YRID-123 MANAGEMENT CODE: F317 BAMAX : 225 -- RUN WICKMANS Y-RIDGE PLOTS WITH VERSION 4.0

STAND COMPOSITION

YEAR	STAND ATTRIBUTES	PERCENTILE POINTS IN THE DISTRIBUTION OF STAND ATTRIBUTES BY DBH (DBH IN INCHES) 10	30	50	70	90	100	TOTAL/ACRE OF STAND ATTRIBUTES	DISTRIBUTION OF STAND ATTRIBUTES BY SPECIES AND 3 USER-DEFINED SUBCLASSES			
1971	TREES	1.8	3.0	4.5	6.8	10.8	27.1	618. TREES	72.% GF1,	21.% DF1,	4.% L1,	2.% PP1
	VOLUME:											
	TOTAL	6.7	9.9	13.7	19.5	27.1	27.1	4345. CUFT	46.% GF1,	29.% DF1,	12.% PP1,	10.% L1
	MERCH	8.6	11.1	17.2	19.8	27.1	27.1	3596. CUFT	42.% GF1,	30.% DF1,	13.% PP1,	10.% L1
	MERCH	10.8	15.1	19.5	20.8	27.1	27.1	14499. BDFT	33.% DF1,	33.% GF1,	16.% PP1,	11.% L1
	ACCRETION	4.8	7.4	9.8	14.2	27.1	27.1	53. CUFT/YR	54.% GF1,	16.% PP1,	14.% L1,	11.% DF1
	MORTALITY	7.1	10.5	13.7	19.5	24.9	27.1	400. CUFT/YR	52.% GF1,	45.% DF1,	2.% PP1,	1.% L1
1976	TREES	1.9	3.1	4.3	6.6	10.2	28.2	382. TREES	66.% GF1,	23.% DF1,	7.% L1,	2.% PP1
	VOLUME:											
	TOTAL	6.4	9.4	13.7	20.2	27.6	28.2	2612. CUFT	42.% GF1,	20.% PP1,	16.% L1,	14.% DF1
	MERCH	8.6	11.1	16.4	20.7	27.6	28.2	2136. CUFT	39.% GF1,	23.% PP1,	18.% L1,	13.% DF1
	MERCH	11.0	14.5	20.0	21.5	27.6	28.2	8647. BDFT	30.% GF1,	27.% PP1,	19.% L1,	13.% S1
	REMOVAL	1.9	3.1	4.3	7.0	10.2	25.2	173. TREES	92.% GF1,	7.% DF1,	1.% GF3,	0.% ---
	VOLUME:											
	TOTAL	6.4	9.0	11.1	16.4	21.1	25.2	989. CUFT	84.% GF1,	16.% DF1,	0.% GF3,	0.% ---
	MERCH	8.3	9.9	11.8	17.5	21.1	25.2	801. CUFT	82.% GF1,	18.% DF1,	0.% ---,	0.% ---
	MERCH	10.1	11.8	16.4	20.4	21.1	25.2	2837. BDFT	79.% GF1,	21.% DF1,	0.% ---,	0.% ---
	RESIDUAL	2.0	3.1	4.3	6.4	10.2	28.2	210. TREES	44.% GF1,	37.% DF1,	12.% L1,	4.% PP1
	ACCRETION	3.9	6.5	8.2	13.5	27.6	28.2	67. CUFT/YR	35.% GF1,	22.% PP1,	20.% DF1,	17.% L1
	MORTALITY	5.9	9.2	14.0	20.2	27.6	28.2	9. CUFT/YR	30.% L1,	29.% PP1,	21.% GF1,	14.% DF1
1981	TREES	2.5	3.8	4.9	7.3	10.9	28.8	202. TREES	44.% GF1,	37.% DF1,	12.% L1,	5.% PP1
	VOLUME:											
	TOTAL	6.7	9.9	14.9	21.1	28.8	28.8	1912. CUFT	30.% PP1,	25.% L1,	20.% GF1,	14.% DF1
	MERCH	8.6	12.5	17.9	28.1	28.8	28.8	1604. CUFT	35.% PP1,	27.% L1,	16.% GF1,	12.% S1
	MERCH	11.1	14.9	21.1	28.6	28.8	28.8	6808. BDFT	39.% PP1,	25.% L1,	18.% S1,	10.% GF1
	ACCRETION	4.0	6.4	8.3	10.9	28.1	28.8	91. CUFT/YR	42.% GF1,	24.% DF1,	17.% PP1,	14.% L1
	MORTALITY	6.0	9.1	14.1	20.6	28.8	28.8	12. CUFT/YR	27.% PP1,	27.% L1,	24.% GF1,	15.% DF1
1991	TREES	4.3	5.4	7.3	9.4	13.3	31.0	186. TREES	44.% GF1,	37.% DF1,	12.% L1,	5.% PP1
	VOLUME:											
	TOTAL	7.5	10.1	14.2	18.6	31.0	31.0	2694. CUFT	27.% GF1,	26.% PP1,	21.% L1,	18.% DF1
	MERCH	9.0	11.1	15.8	22.0	31.0	31.0	2329. CUFT	29.% PP1,	26.% GF1,	22.% L1,	13.% DF1
	MERCH	10.4	14.3	18.5	29.0	31.0	31.0	10030. BDFT	33.% PP1,	23.% L1,	20.% GF1,	14.% S1
	ACCRETION	5.3	7.9	9.8	11.9	18.6	31.0	104. CUFT/YR	46.% GF1,	25.% DF1,	13.% L1,	11.% PP1
	MORTALITY	6.7	9.9	13.6	18.5	31.0	31.0	19. CUFT/YR	30.% GF1,	24.% PP1,	22.% L1,	18.% DF1

2001	TREES	5.7	7.2	9.0	11.1	15.0	32.2	171.	TREES	44.% GF1,	37.% DF1,	12.% L1,	5.% PP1
	VOLUME:												
	TOTAL	8.1	11.3	14.0	18.5	32.2	32.2	3544.	CUFT	33.% GF1,	22.% PP1,	20.% DF1,	19.% L1
	MERCH	9.5	11.8	14.7	19.3	32.2	32.2	3181.	CUFT	33.% GF1,	23.% PP1,	19.% L1,	16.% DF1
	MERCH	10.8	13.5	17.2	24.3	32.2	32.2	13915.	BDFT	29.% GF1,	27.% PP1,	21.% L1,	12.% DF1
	ACCRETION	7.0	9.7	11.6	14.0	19.3	32.2	110.	CUFT/YR	52.% GF1,	23.% DF1,	12.% PP1,	10.% L1
	MORTALITY	8.0	11.2	14.0	17.4	31.2	32.2	27.	CUFT/YR	35.% GF1,	20.% PP1,	19.% DF1,	19.% L1
2006	TREES	6.0	7.6	9.6	11.8	15.9	32.8	164.	TREES	44.% GF1,	37.% DF1,	12.% L1,	5.% PP1
	VOLUME:												
	TOTAL	8.7	11.7	14.8	18.2	31.9	32.8	3962.	CUFT	35.% GF1,	20.% PP1,	20.% DF1,	17.% L1
	MERCH	9.5	12.3	15.3	18.6	32.8	32.8	3612.	CUFT	36.% GF1,	22.% PP1,	18.% L1,	17.% DF1
	MERCH	10.7	13.8	17.0	24.4	32.8	32.8	16175.	BDFT	33.% GF1,	25.% PP1,	19.% L1,	13.% DF1
	ACCRETION	7.2	10.5	13.0	17.0	31.9	32.8	57.	CUFT/YR	30.% GF1,	23.% PP1,	22.% L1,	18.% DF1
	MORTALITY	9.1	11.5	13.9	15.9	18.2	32.8	239.	CUFT/YR	60.% GF1,	33.% DF1,	3.% PP1,	2.% L1
2011	TREES	6.2	7.5	9.5	11.6	16.9	33.4	109.	TREES	37.% DF1,	34.% GF1,	18.% L1,	7.% PP1
	VOLUME:												
	TOTAL	8.7	12.2	15.7	20.9	33.4	33.4	3050.	CUFT	27.% PP1,	24.% GF1,	24.% L1,	15.% DF1
	MERCH	9.5	12.8	16.7	25.0	33.4	33.4	2802.	CUFT	29.% PP1,	25.% L1,	25.% GF1,	11.% DF1
	MERCH	11.5	14.2	18.6	25.3	33.4	33.4	12981.	BDFT	33.% PP1,	25.% L1,	22.% GF1,	13.% S1
	REMOVAL	6.4	9.0	10.7	12.4	16.5	32.7	29.	TREES	75.% GF1,	24.% DF1,	2.% GF3,	0.% ---
	VOLUME:												
	TOTAL	9.2	11.3	13.9	16.5	18.6	32.7	647.	CUFT	80.% GF1,	19.% DF1,	1.% GF3,	0.% ---
	MERCH	9.5	11.9	14.3	16.5	18.6	32.7	599.	CUFT	81.% GF1,	18.% DF1,	1.% GF3,	0.% ---
	MERCH	10.8	12.8	15.2	16.7	18.8	32.7	2582.	BDFT	83.% GF1,	16.% DF1,	1.% GF3,	0.% ---
	RESIDUAL	6.1	7.3	9.0	11.5	17.6	33.4	80.	TREES	42.% DF1,	25.% L1,	19.% GF1,	9.% PP1
	ACCRETION	6.8	9.3	11.6	13.8	25.4	33.4	62.	CUFT/YR	27.% DF1,	24.% PP1,	23.% GF1,	21.% L1
	MORTALITY	8.3	12.3	17.4	25.0	33.4	33.4	12.	CUFT/YR	36.% L1,	32.% PP1,	13.% DF1,	12.% GF1
2021	TREES	7.0	8.4	10.4	13.0	18.5	34.7	76.	TREES	43.% DF1,	24.% L1,	19.% GF1,	9.% PP1
	VOLUME:												
	TOTAL	8.8	13.2	17.0	26.0	34.7	34.7	2907.	CUFT	33.% PP1,	28.% L1,	17.% DF1,	12.% GF1
	MERCH	9.6	13.6	18.1	26.0	34.7	34.7	2743.	CUFT	34.% PP1,	28.% L1,	15.% DF1,	12.% GF1
	MERCH	12.4	15.3	20.4	26.8	34.7	34.7	12857.	BDFT	38.% PP1,	29.% L1,	14.% S1,	11.% GF1

Figure 6.—Sample Stand Prognosis output from the Combined Model: Stand Table.

STAND GROWTH PROGNOSIS SYSTEM VERSION 4.0 -- INLAND EMPIRE

STAND ID; YRID-123 MANAGEMENT CODE: F3T7 BAMAX = 220 -- RUN WICKMANS Y-RIDGE PLOTS WITH VERSION 4.0

	ATTRIBUTES OF SELECTED SAMPLE TREES								ADDITIONAL STAND ATTRIBUTES					
YEAR	INITIAL TREES/A %TILE	SPECIES	DBH (INCHES)	HEIGHT (FEET)	LIVE CROWN RATIO	PAST DBH GROWTH (INCHES)	BASAL AREA %TILE	TREES PER ACRE	STAND AGE	QUADRATIC MEAN DBH (INCHES)	TREES PER ACRE	BASAL AREA (SQFT/A)	HEIGHT OF DOMINANTS (FEET)	CROWN COMP FACTOR
1971						(10 YRS)								
	10	GF1	1.80	10.17	32	0.0	0.3	2.50						
	30	GF1	3.00	18.15	19	0.0	2.7	2.50						
	50	GF1	4.50	28.36	17	0.0	8.0	2.50						
	70	GF1	6.80	41.53	35	0.90	20.8	2.50						
	90	DF1	10.80	62.69	60	0.0	49.9	2.50						
	100	PP1	27.10	103.67	29	0.0	100.0	2.50						
									50	7.2	618.	173.	90.2	214.8
1976						(5 YRS)								
	10	GF1	2.01	11.90	32	0.19	0.5	1.84						
	30	GF1	3.15	20.28	23	0.14	3.4	1.11						
	50	GF1	4.69	30.94	22	0.17	10.7	1.84						
	70	GF1	7.07	44.63	40	0.25	24.8	1.84						
	90	DF1	11.10	65.55	63	0.26	56.3	2.31						
	100	PP1	27.62	106.14	34	0.46	97.4	2.35						
									55	6.9	382.	99.	94.0	122.8
								RESIDUAL:		7.1	210.	57.	103.4	63.0
1981						(5 YRS)								
	10	GF1	2.63	15.89	32	0.56	0.7	1.76						
	30	GF1	3.44	24.84	24	0.27	2.8	0.02						
	50	GF1	5.78	36.53	25	0.99	12.9	0.04						
	70	GF1	8.07	50.41	43	0.91	30.4	0.04						
	90	DF1	12.46	70.97	66	1.18	55.2	2.25						
	100	PP1	28.85	109.58	37	1.09	100.0	2.29						
									60	7.7	202.	65.	106.0	71.9
1991						(10 YRS)								
	10	GF1	4.95	24.41	38	2.13	3.4	1.59						
	30	GF1	5.21	34.53	26	1.62	4.9	0.02						
	50	GF1	7.58	47.11	26	1.65	17.6	0.03						
	70	GF1	9.78	61.12	43	1.56	36.5	0.03						
	90	DF1	15.06	81.09	67	2.25	66.7	2.12						
	100	PP1	31.01	115.82	37	1.92	100.0	2.16						
									70	9.3	186.	88.	104.8	97.3

2001					(10 YRS)								
10	GF1	6.52	33.17	39	1.44	5.7	1.45						
30	GF1	8.47	45.51	31	2.98	17.2	0.02						
50	GF1	9.39	57.66	27	1.65	22.5	0.03						
70	GF1	11.66	71.58	44	1.72	43.0	0.03						
90	DF1	17.04	88.99	67	1.71	72.5	1.97						
100	PP1	32.22	120.29	37	1.08	100.0	2.02	80	10.8	171.	109.	105.1	116.8
2006					(5 YRS)								
10	GF1	7.46	38.13	39	0.85	8.3	1.39						
30	GF1	9.18	50.26	30	0.65	17.7	0.02						
50	GF1	9.75	61.25	26	0.33	21.7	0.03						
70	GF1	12.44	76.08	43	0.72	43.8	0.03						
90	DF1	18.18	92.75	67	0.99	78.8	1.90						
100	PP1	32.80	122.34	36	0.51	100.0	1.94	85	11.5	164.	118.	107.4	123.5
2011					(5 YRS)								
10	GF1	7.75	41.86	42	0.27	10.6	0.62						
30	GF1	9.82	54.88	33	0.59	21.1	0.02						
50	GF1	10.38	65.29	28	0.58	23.4	0.02						
70	GF1	12.82	79.70	46	0.35	44.3	0.00						
90	DF1	18.61	95.57	68	0.37	70.8	0.78						
100	PP1	33.42	124.40	38	0.55	100.0	1.87	90	11.8	109.	83.	114.2	81.7
								RESIDUAL:	11.9	80.	62.	118.4	56.4
2021					(10 YRS)								
10	GF1	9.10	51.91	42	1.24	13.9	0.01						
30	GF1	11.33	64.56	33	1.39	25.7	0.01						
50	GF1	11.19	72.38	28	0.74	22.8	0.02						
70	GF1	13.96	87.30	46	1.04	43.3	0.00						
90	DF1	19.84	100.99	68	1.07	67.2	0.01						
100	PP1	34.71	128.46	38	1.15	100.0	1.78	100	13.1	76.	71.	122.4	64.0

Figure 7.—Sample Stand Prognosis output from the Combined Model: Sample Tree Summary Table.

BEHAVIOR OF THE COMBINED MODEL

The purpose of this section is to illustrate the behavior of the Combined Model when the major input options are varied. This section does not purport to be a sensitivity analysis, however. In all figures in this section, simulated stand volume development is plotted against time over the course of a 50- to 100-year projection, using the same stand. The sample stand simulated is B. E. Wickman's Y-Ridge plots 1, 2, and 3, as measured at the beginning of the 1971-74 Oregon Blue Mountains outbreak. This stand is two-storied with 70 percent of the trees less than 6.8 inches d.b.h. in 1971 (before the outbreak). The two host species for tussock moth comprise most of the stand: grand fir and Douglas-fir account for 72 and 21 percent of the trees per acre and 46 and 29 percent of the total volume in 1971, respectively.

The "no outbreak" curve will be the same on all figures, and indicates what the expected volume development over time would be for this stand if an outbreak had not occurred. Since the version of the Stand Prognosis Model used in this analysis did not include regeneration establishment, all simulation results reported here are based on projecting only trees and seedlings already established at the start of the outbreak. Thus, the simulations that produced heavy mortality or large salvage removals quite likely underestimate stand volume near the end of the 50-year projections.

Keep in mind that these examples are projections into the future, which obviously involves considerable uncertainty; our best guess should never be confused with certainty. Also keep in mind that this one sample stand (or any one stand) is unlikely to be typical of an area as large and diverse as the Blue Mountains of Oregon and Washington.

The reader should note that the figures to be presented in this section differ from and supersede the figures Monserud (1978b) presented with a preliminary description of the Combined Model. There are several reasons for the differences: (1) significant changes have been made to the Stand Prognosis Model since 1978, especially in the mortality model and to a lesser extent in the diameter growth model (Monserud 1978b used North Idaho version 2.1, whereas Inland Empire Version 4.0 was used for this paper); (2) changes have also been made in the subroutines that link the Stand Prognosis Model with the DFTM Outbreak Model, especially in the tree class compression algorithm; and (3) Monserud (1978b) used Wickman's Y-Ridge plots 1-4, whereas the examples simulated in this section are based only on plots 1-3.

Figures 8-12 illustrate the effect of varying the method for allocating first instar larvae to the tree classes at the start of the outbreak. In figure 8, the random larval allocation assumption (see the RANLARVA keyword) was used to allocate an average of 5, 8, 14, 20, and 100 first instar larvae per 1000-in^2 sample branch, using a standard deviation of 2 larvae in all cases. Only minor impacts on projected stand volume resulted when larval densities averaged 5 or less per 1000-in^2 sample branch for each tree class. Severity increased when this average density increased to 8, with 670 ft^3/acre lost in 5 years. At an average density of 14 larvae, over 40 percent of the standing volume was lost in 5 years. Increasing the average initial number of larvae from 14 to 20 resulted in a relatively small increase in the severity of the outbreak: 650 ft^3/acre more were lost in 5 years. Note the nonlinear effect on volume lost as average larval density is increased. The change in volume loss attributable to increasing average density from 8 to 14 larvae per tree class is over two times the change in volume loss due to increasing density from 14 to 20 larvae per tree class. And perhaps the highly nonlinear behavior of the DFTM Outbreak Model is best illustrated by observing the effect of increasing the average number of larvae to the highly unlikely level of 100; insect densities were so high that there was not enough new foliage to carry the population through the first two instars. Mass starvation ensued, resulting in the collapse of the simulated outbreak.

After 45 years, projected volume development following the lowest two levels of outbreak (5 and 8 larvae per tree class) illustrated in figure 8 nearly caught up with the no-outbreak volume level. However, even 50 years after the two most severe simulated outbreaks began (14 and 20 larvae), volume development was still 700 to 1300 ft³/acre behind the no-outbreak level. Obviously, insect density at the start of the outbreak can influence the simulated stand's development far into the projection.

This figure illustrates an additional important point. Consider one of the most severe outbreaks graphed, the 14 larvae per tree class curve. Five years after the outbreak began, almost 2000 ft³/acre were estimated to be lost. But 50 years after the outbreak began, only 700 ft³/acre were lost (and probably less than that since any regeneration subsequent to the outbreak was ignored). If this particular stand were not scheduled for harvest for, say, 50 years, then it is misleading to tell the manager that 2000 ft³/acre have been lost, for the stand will probably "find" much more than half of these lost cubic feet if left alone for 45 more years. The point of this admittedly oversimplified argument is that "loss" is not constant over time. Perhaps more realistic measures of loss would be either the expected number of additional years required to reach the volume anticipated at the end of the rotation if there had been no tussock moth outbreak, or the expected volume loss at the end of the scheduled rotation.

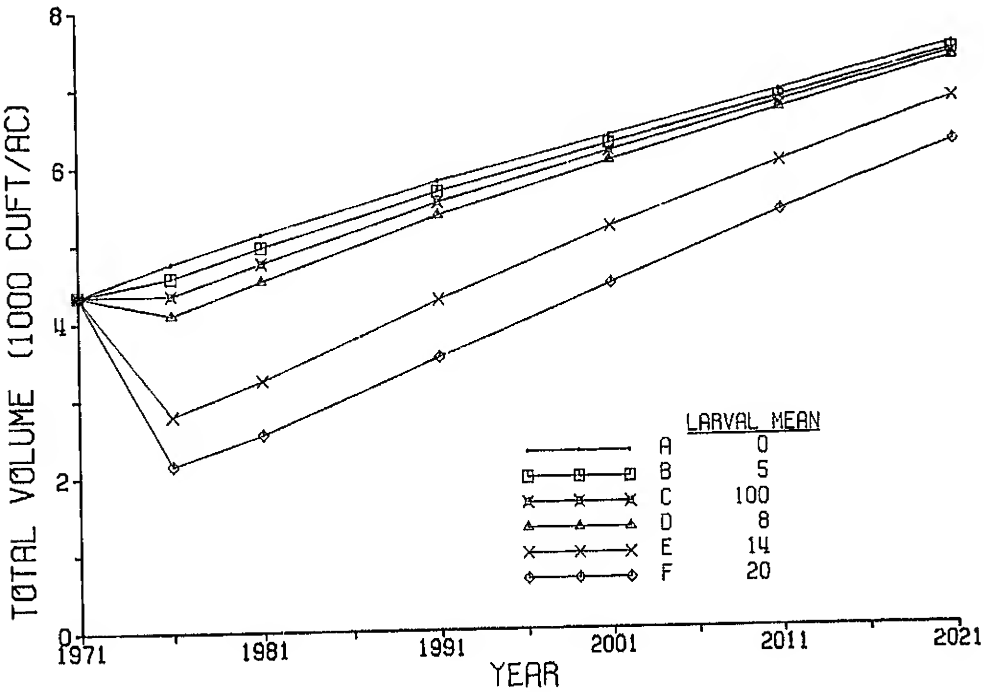

Figure 8.—Comparison of simulated volume development resulting from outbreaks beginning with an average of 5, 8, 14, 20, and 100 first instar larvae per tree class. Larvae were randomly allocated (using RANLARVA) with a within-outbreak standard deviation of 2 larvae.

The random larval allocation assumption is also used in figures 9 and 10, but with the within-outbreak standard deviation of larvae varying (Field 3 on the RANLARVA keyword record) rather than the average number of larvae per tree class. The average number of larvae in these simulations was 14 for figure 9, and 5 for figure 10; standard deviations of 0, 2, 4, 8, and 16 larvae per tree class were used for both figures. Examination of figures 9 and 10 indicates that the relationship between the severity of the outbreak and the variability of the larval density (judging from the standard deviation about the average level) depends somewhat on the average density of the larvae. When the average density is low (figure 10: 5 larvae per tree class), severity increases as larval variability increases; this effect is somewhat reversed when average density is high (figure 9: 14 larvae per tree class). The reason for this behavior is actually illustrated in figure 8. When the average larval density is high, the increase in severity (volume loss) on tree classes that received positive random deviates (more insects than the average) in the larval allocation procedure is more than offset by the decrease in severity on tree classes receiving equally likely negative deviates. And when larval density is low, the opposite effect occurs, for a positive deviate when randomly allocating larvae to tree classes results in much more volume loss than can be gained by an equally sized negative deviate.

The effect of allocating a fixed amount of first instar larvae to trees in three different size classes is compared next (figures 11 and 12); the deterministic larval allocation assumption (see the DETLARVA keyword) is used to simulate this. Recall that tree classes are sorted by average diameter into descending order before larvae are allocated deterministically. The high, medium, and low larval levels were 11, 9, and 7 for Douglas-fir sample branches and 15, 10, and 5 for grand fir, respectively; the default values of all other options were used.

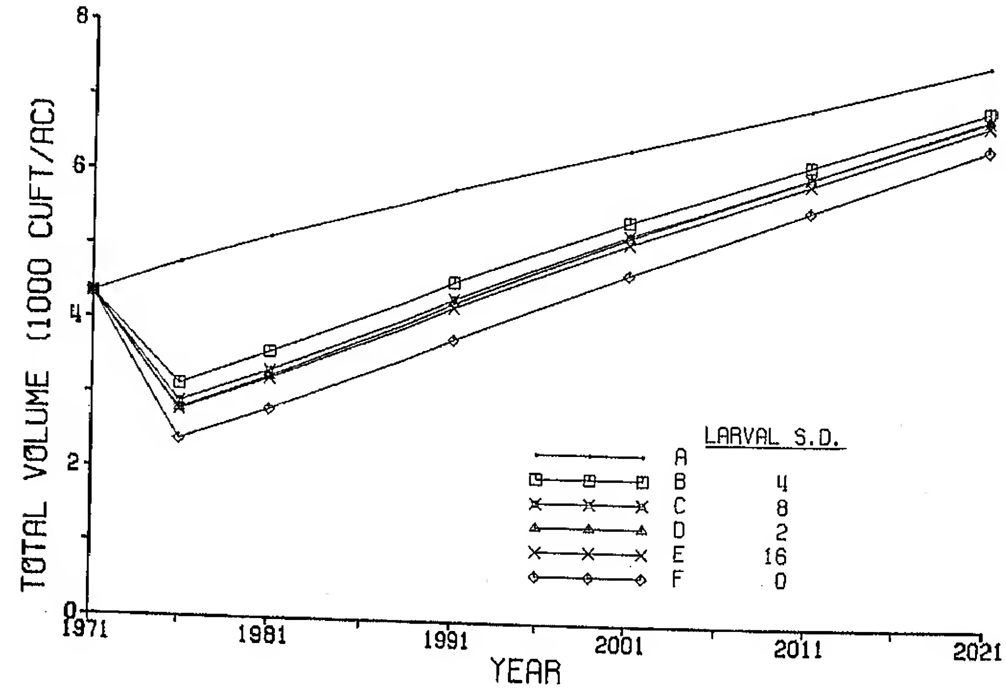

Figure 9.—Simulated volume development resulting from outbreaks beginning with average of 14 first instar larvae per tree class. Larvae were randomly allocated with andard deviation of 0, 2, 4, 8, and 16 larvae.

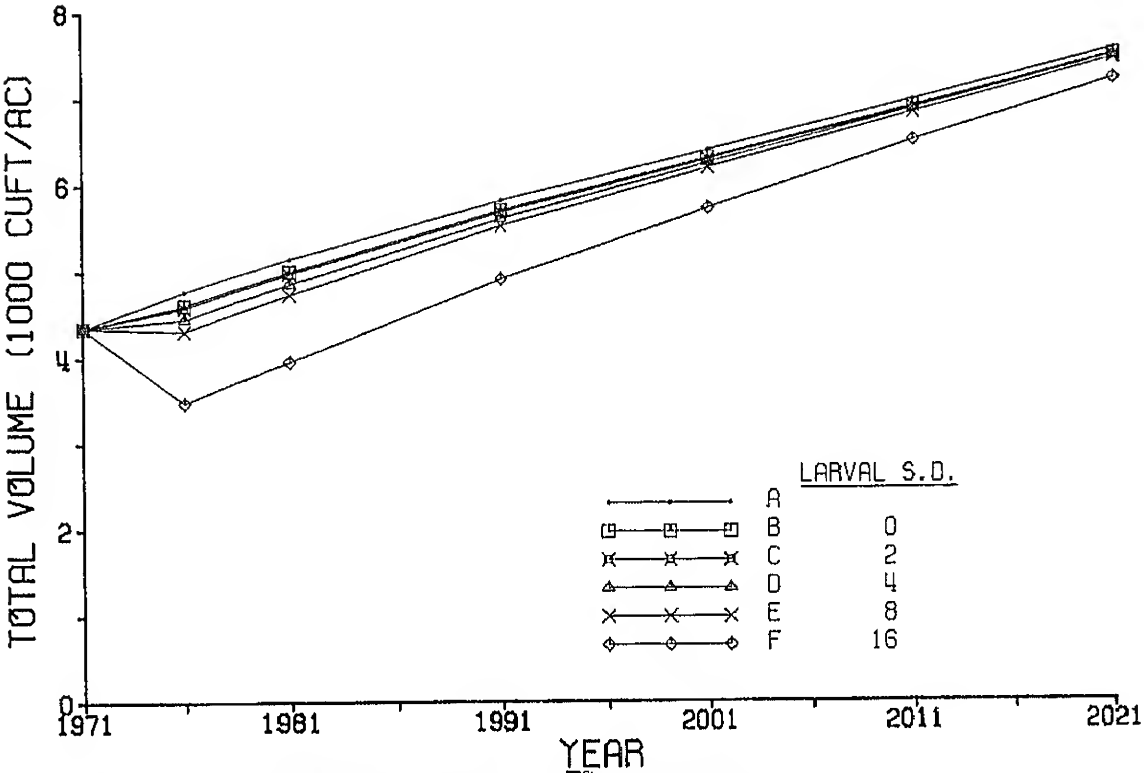

Figure 10.—Simulated volume development resulting from outbreaks beginning with an average of 5 first instar larvae per tree class. Larvae were randomly allocated with a standard deviation of 0, 2, 4, 8, and 16 larvae.

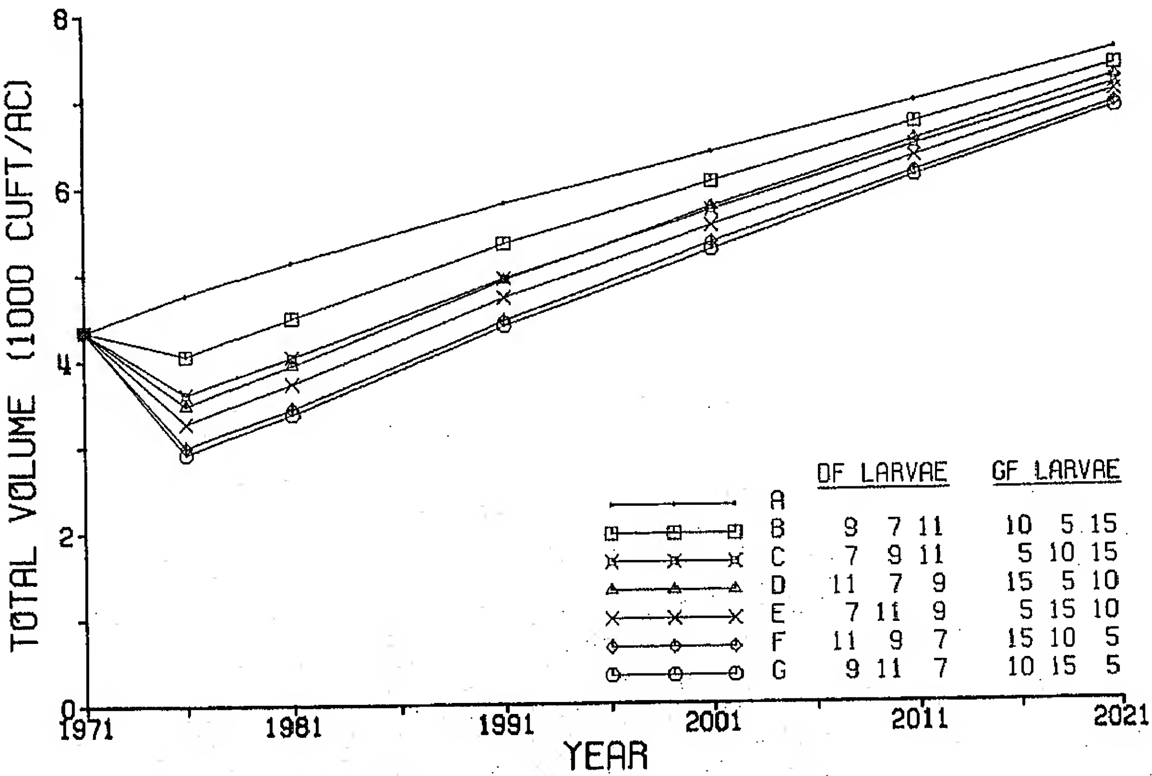

Figure 11.—Simulated volume development following outbreaks resulting from deterministically allocating three larval densities (Douglas-fir: 7, 9, 11; grand fir: 5, 10, 15) to each third of the average diameter distribution. Each outbreak resulted from the same total number of first instar larvae. Note that each tree class represented an unequal number of trees per acre.

All possible combinations of allocating these larval densities to the three diameter classes were simulated to produce figure 11. The most severe reduction in volume was obtained by assigning the high larval density to the middle third rather than the top third of the diameter distribution. This apparent anomaly occurred because the middle third of the diameter distribution represents more trees per acre (and more volume) than the upper third. In light of this, it is not surprising that the least severe reductions in volume resulted from assigning the low larval density to the middle third of the diameter distribution. Recall that the number of trees per acre each tree class represents is determined both by the original stand inventory design and the method for allocating tree records to tree classes (Field 3 on the NUMCLASS keyword record); the methods for allocating larvae to the tree classes are independent of the number of trees per tree class.

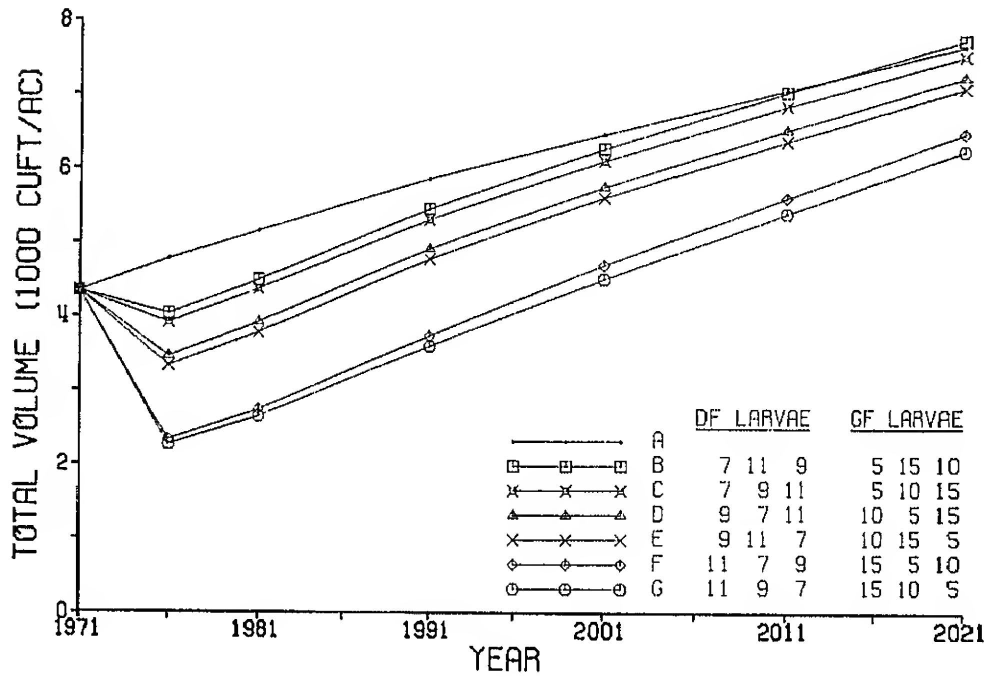

Figure 12.—Simulated volume development following outbreaks resulting from deterministically allocating three larval densities (Douglas-fir: 7, 9, 11; grand fir: 5, 10, 15) to each third of the average diameter distribution; each tree class represents approximately an equal number of trees per acre. Each outbreak resulted from the same total number of first instar larvae.

In the simulations illustrated in figure 12, larvae were allocated deterministically to tree classes exactly as they were in figure 11. For this case, however, biomass was allocated deterministically (using BIOMASS method 3 rather than the default method 4), and the successive-halving rule was used exclusively to create tree classes (Field 3 was 0.0 on the NUMCLASS keyword). These two changes resulted in an approximately equal number of tree records in each tree class, and thus the number of trees per acre in each third of the diameter distribution was roughly equal. The result of varying the allocation of a fixed number of larvae by tree size-class can be quite dramatic, as can be seen in figure 12. As expected, the most severe outbreaks (judging from volume loss) occur when the high level of larvae are assigned to the largest third of the diameter class, and the least severe outbreaks occur when this high level of insects is distributed to the lowest third of the diameter class.

This latter case is quite interesting, for the standing volume 45 years after the lightest outbreak (curve B in figure 12) is greater than in the "no outbreak" simulation, even though 740 ft^3/acre were killed by the tussock moth in this outbreak. Concentrating the larvae in the smaller diameter trees is apparently silviculturally similar (in this case) to a light thinning in a stand that is overstocked in the small diameter classes. Although tussock moth outbreaks invariably result in a short-term volume loss, these results indicate that some outbreaks have the potential for mimicking wise management, and being beneficial in the long

run. It is quite apparent from figure 12 that stand volume development can vary greatly, depending on the size of tree defoliated during the outbreak. Using overall stand averages for insect densities thus results in less precise estimates of volume development if the pest is differentiating between tree size classes, or redistributing more to trees of one size class than another.

The effect of varying the method of allocating foliage biomass to the tree classes is examined next (fig. 13). In this and subsequent runs, the random larvae option was used to allocate an average of 14 first instar larvae per tree class, with a standard deviation of 2 larvae. A fairly large amount of variability results from varying the foliage biomass method. This should not be surprising, for foliage biomass is the only tree characteristic important to the DFTM Outbreak Model. Note, however, that all the outbreak volume-over-time curves in figure 13 converge, except that which was produced by using BIOMASS method 2 (curve B); this method uses the deterministic biomass equations of Hatch and Mika (1978) that Monserud (1978a) concluded are poorly behaved.

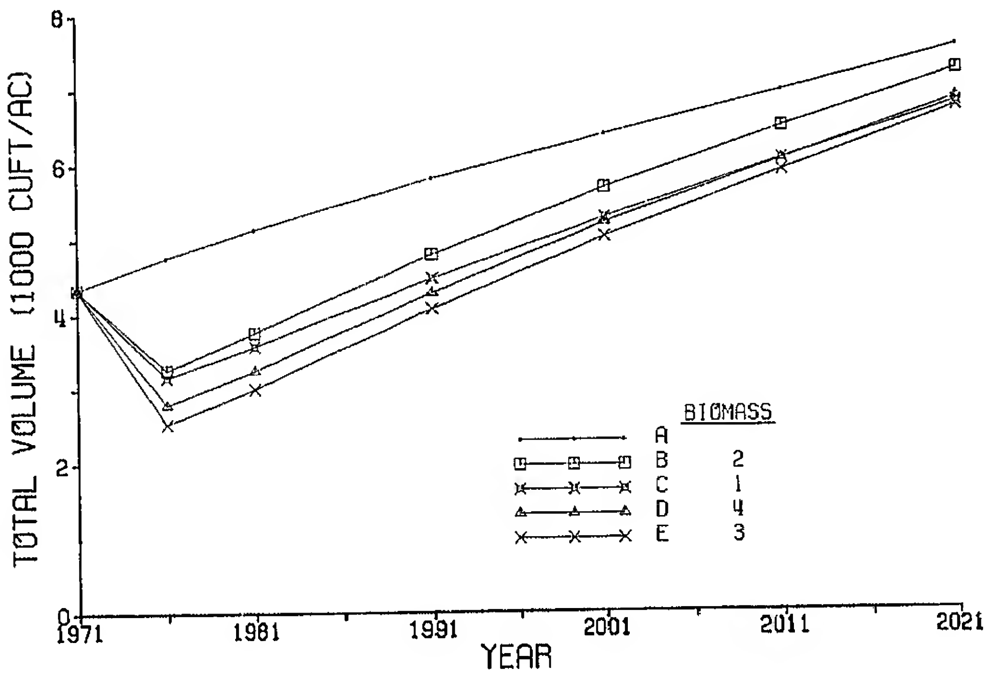

Figure 13.—Comparison of simulated volume development resulting from outbreaks that began with each of the four methods of allocating foliage to the 1000-in² midcrown sample branch that represents a tree class. In this and all subsequent figures, the random allocation method was used to distribute an average of 14 first instar larvae per tree class, with a within-outbreak standard deviation of 2 larvae, except for figures 22 and 24. In addition, the default foliage biomass option (method 4) was used for all other figures.

Figure 14 illustrates the effectiveness of simulating various control measures for the same outbreak conditions. The "no control" curve (G) in figure 14 is the same as curve E in figure 8 and curve D in figure 13: foliage was determined by the default biomass option (method 4), and first instar larvae were assigned to tree classes randomly (average = 14, standard deviation = 2). Control treatments (especially virus) that are applied in Phase II of this simulated outbreak almost completely control the tussock moth (as far as volume loss is concerned), unless the treatment is of low efficacy (e.g., 80 percent) and applied late in

Phase II (curve C). Delaying control treatments until Phase III results in much greater variation in effectiveness. An early application of chemical control with a high efficacy (e.g., 95 percent, curve B) is quite effective in reducing volume loss, while delaying application until late in the outbreak results in almost no control even through efficacy is high (curve F). Intermediate levels of control are obtained by applying virus (curve E) or chemical controls of lower efficacy (curve D) early in Phase III. All simulated control measures had one obvious effect in common: the later the application and/or the lower the efficacy, then the greater the volume loss at the end of the outbreak.

The effect of varying salvage intensities is next shown (fig. 15). Note that the "no salvage" outbreak curve (B) is the same as the "no control" curve (G) in figure 14. The major effect of salvage appears to be a reduction in the rate of stand development; the rate of reduction increases as salvage intensity increases. Keep in mind that the volume available at the end of these 50-year projections is most likely underestimated for the heavy salvage treatments, because the current version of the Stand Prognosis Model does not yet simulate the development of seedlings that would become established subsequent to the salvage. It is apparent, however, that the time required for a simulated stand to reach preoutbreak volume levels can be lengthened considerably by increasing the salvage intensity.

In figure 16 the annual insect redistribution rate (Field 1 on the REDIST keyword record) is varied. As in previous figures, first instar larvae at the start of the outbreak were allocated to tree classes randomly with a mean of 14 and a standard deviation of 2 larvae per tree class. As expected, the severity of the outbreak increases as the insect redistribution rate is increased from 0.0 (no annual insect redistribution) to 1.0 (completely uniform redistribution of insects among tree classes). Although not illustrated, varying the redistribution rate with a higher standard deviation (namely 8) for allocating larvae to tree classes produced essentially the same results as exhibited in figure 16.

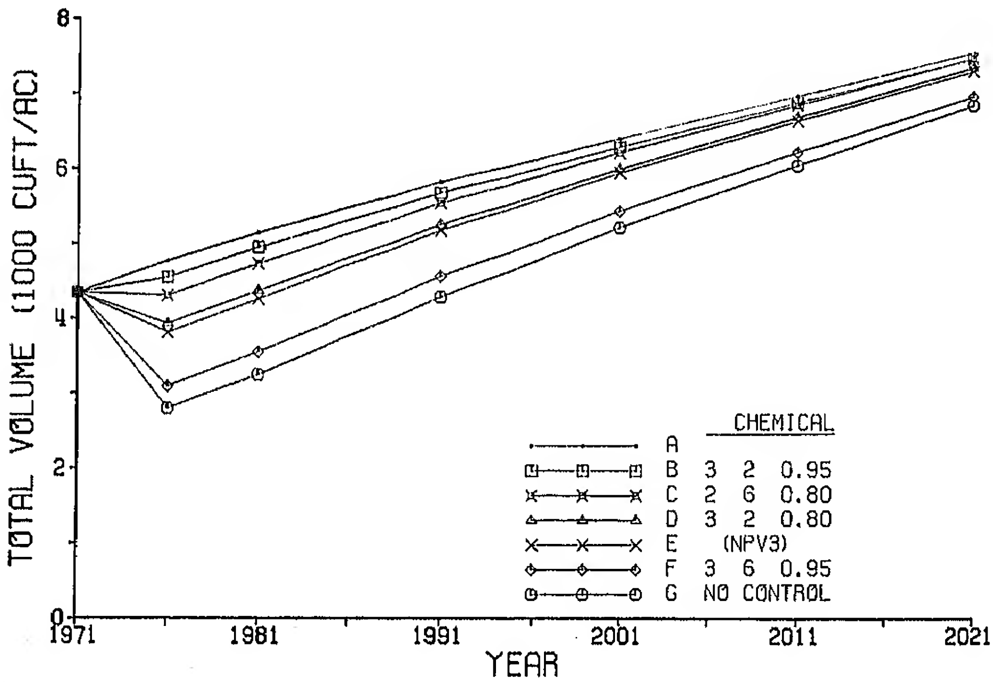

Figure 14.—Simulated volume development following application of various DFTM control measures. Virus and chemical controls applied in Phase II or III were simulated. In addition, two efficacy levels (80 percent and 95 percent) and early (instar 2) and late (instar 5) application of chemical control were considered.

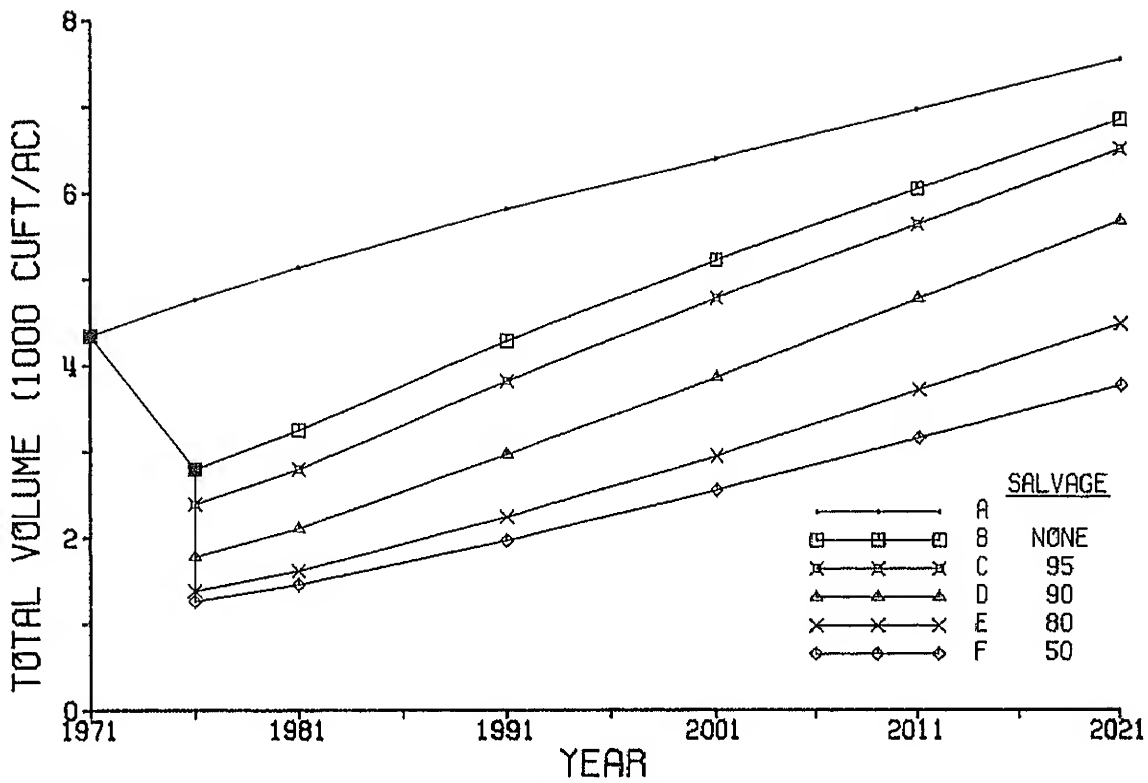

Figure 15.—Simulated volume development following various salvage intensities. Surviving trees with defoliation exceeding 95 percent, 90 percent, 80 percent, and 50 percent were salvaged. Note that an additional 1835 ft³/acre in mortality is also available for salvage in 1976.

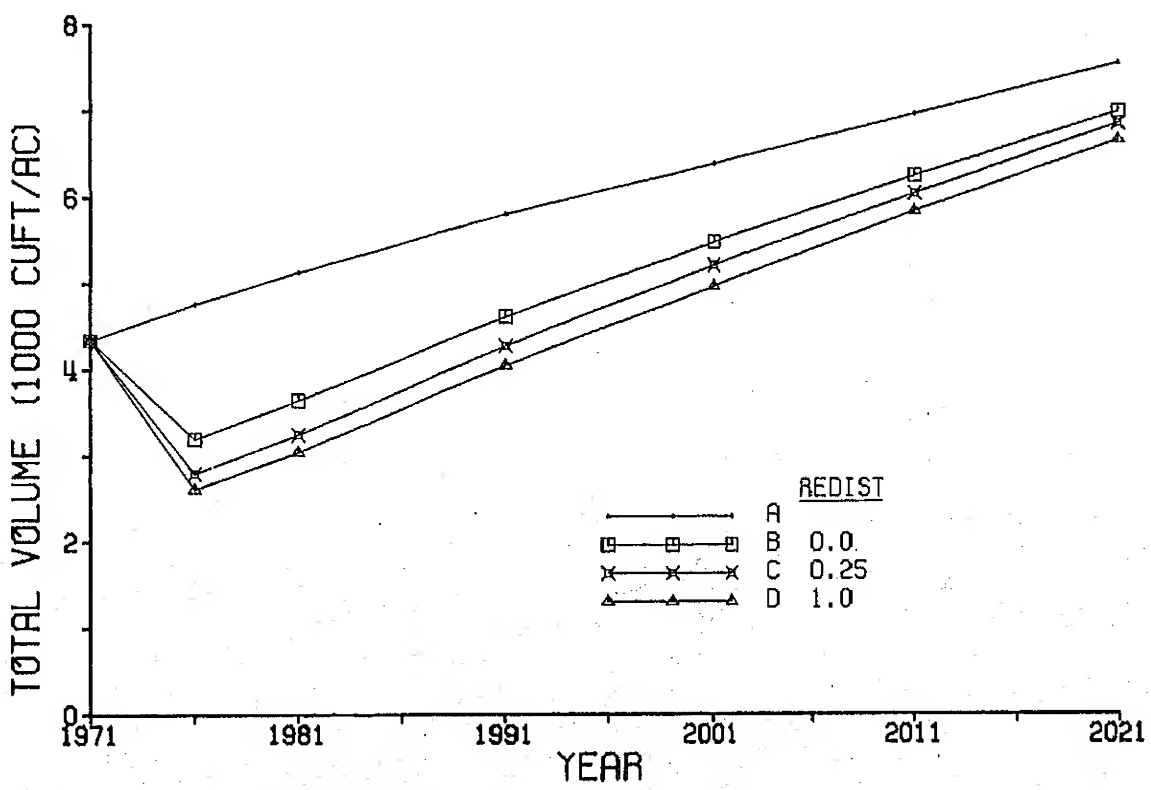

Figure 16.—Simulated volume development resulting from varying the annual insect redistribution rate during the outbreak. A rate of 0.0 results in no redistribution, and a rate of 1.0 results in perfectly uniform redistribution of insects among tree classes; the default value is 0.25.

In figures 17 though 20, the factors that affect the compression of the list of trees into tree classes are varied. The WEIGHT keyword is used to specify the relative importance of the two foliage biomass variables (i.e., percentage new foliage and total foliage biomass of the sample branch). Curve C in figure 17 was produced by the default values for the WEIGHT keyword parameters: percentage new foliage and total foliage biomass both had a weight of 1.0 (i.e., percentage new foliage was considered just as important as total foliage biomass). Most combinations of WEIGHT keyword parameters produced simulated results that are bracketed by the two extremes: giving percentage new foliage no weight (curve B), and giving total foliage biomass no weight (curve F) in the tree class compression routine. An examination of figure 17 reveals that varying the parameters of the WEIGHT keyword resulted in minor changes in predicted volume for this particular stand. This is primarily a result of the method of allocating the foliage biomass to the trees (method 4 in this case). As long as there is a strong correlation between percentage foliage biomass and total foliage biomass, then changing the parameters on the WEIGHT keyword should have a minor effect on the simulated outbreak.

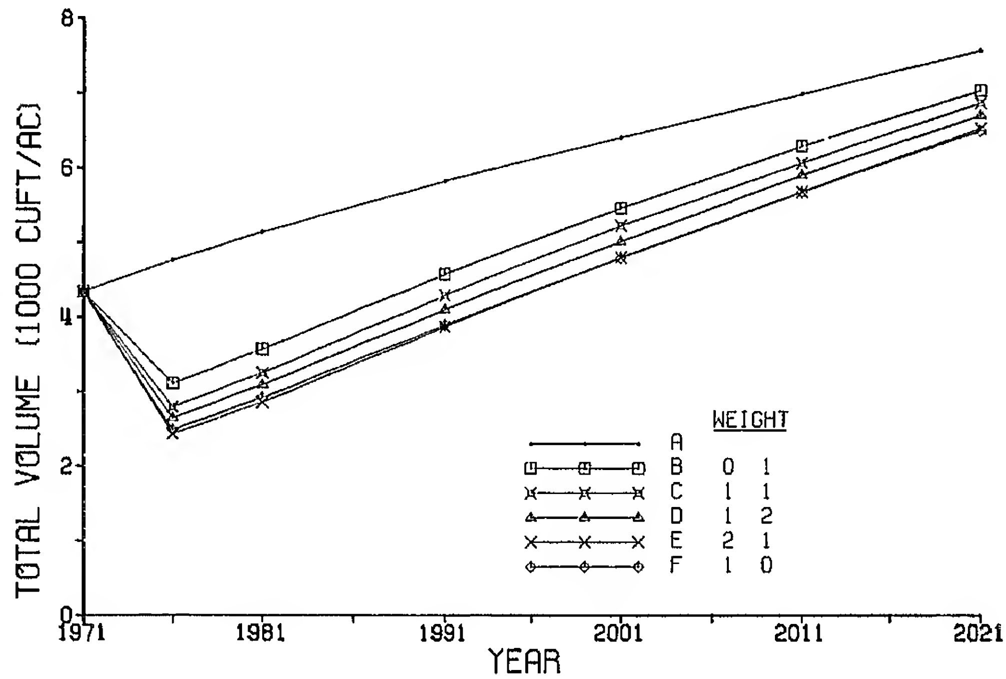

Figure 17.—Simulated volume development resulting from varying the parameters on the WEIGHT keyword that determine the importance of percentage new foliage relative to total foliage biomass in the tree class compression algorithm.

The number of tree classes (the first two parameters of the NUMCLASS keyword) used to represent the list of trees in the DFTM Outbreak Model is next varied (fig. 18). Observe that the default values of 20 tree classes per host species (curve C) result in a volume-over-time curve that is quite close to the curve produced by using 50 tree classes per species (curve D). Based on numerous projections, 20 tree classes per species does appear to provide a good approximation to the actual tree list. Note that using 5 tree classes per species (curve B) resulted in a volume-over-time curve almost coincident with the default 20 tree class per species curve (C). It would be incorrect, however, to infer that using 5 tree classes per species is as accurate as using 20 (although it is true in the example summarized by figure 18). Generally, using less than 10 tree classes per species results in quite erratic behavior, and is not recommended.

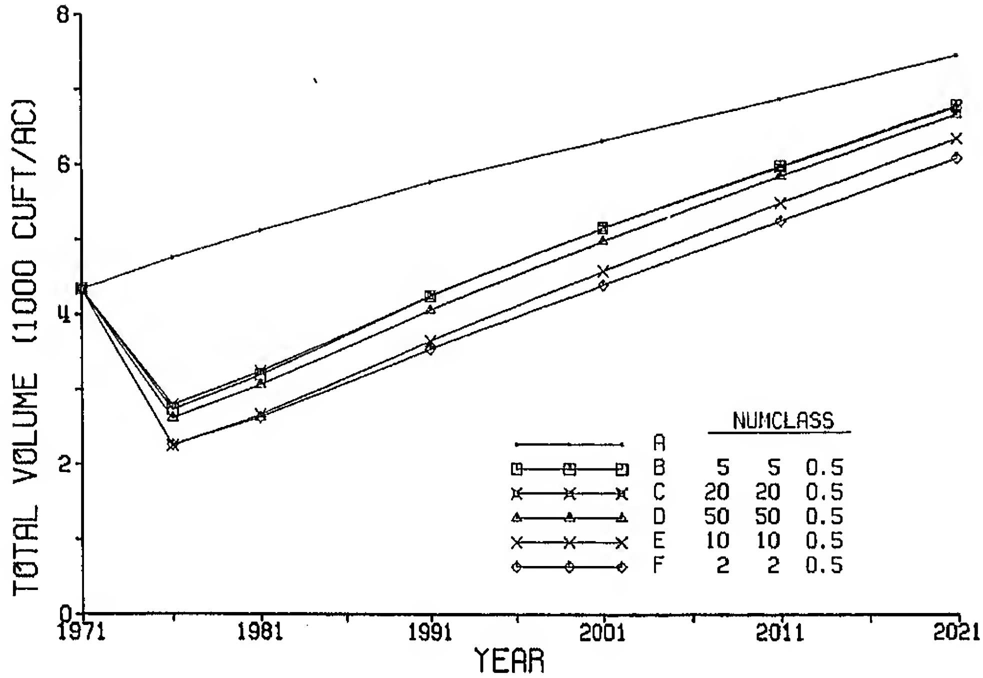

Figure 18.—Simulated volume development resulting from varying the number of tree classes into which the list of trees is compressed before calling the DFTM Outbreak Model. Half of the tree classes were created using the (first) maximum difference algorithm, and the remainder were created by the (second) successive halving compression algorithm.

The third parameter (temporarily call it PROP) on the NUMCLASS keyword record specifies the proportion of tree classes to be determined by the first tree class compression algorithm (the maximum difference algorithm); the remainder are created using the second (successive halving) algorithm. To see the effect of varying PROP as the number of tree classes per species is also varied, compare figure 19 (using PROP = 0: the successive halving algorithm) and figure 20 (using PROP = 1: the maximum difference algorithm) with figure 18 (PROP = 0.5, the default). It is apparent that exclusive use of the maximum difference algorithm (fig. 20) results in large variation in the consequent simulated outbreak as the number of tree classes is varied; the volume-over-time curve does not stabilize until the number of tree classes gets close to 50 per species. In contrast, the second compression algorithm (used exclusively in figure 19) produces stable results with much fewer tree classes (and less computing cost).

Results obtained from simulated outbreaks that utilize the pseudorandom number generator (Marsaglia and Bray 1968) are obviously conditional upon the sequence of random numbers used in the various calculations. The amount of variability in a given simulation that is due to the random number sequence is not at all obvious, however. By reseeding a given simulation several times (with the RANNSEED keyword) and holding all other input conditions constant, this "random" variability can be isolated and assessed.

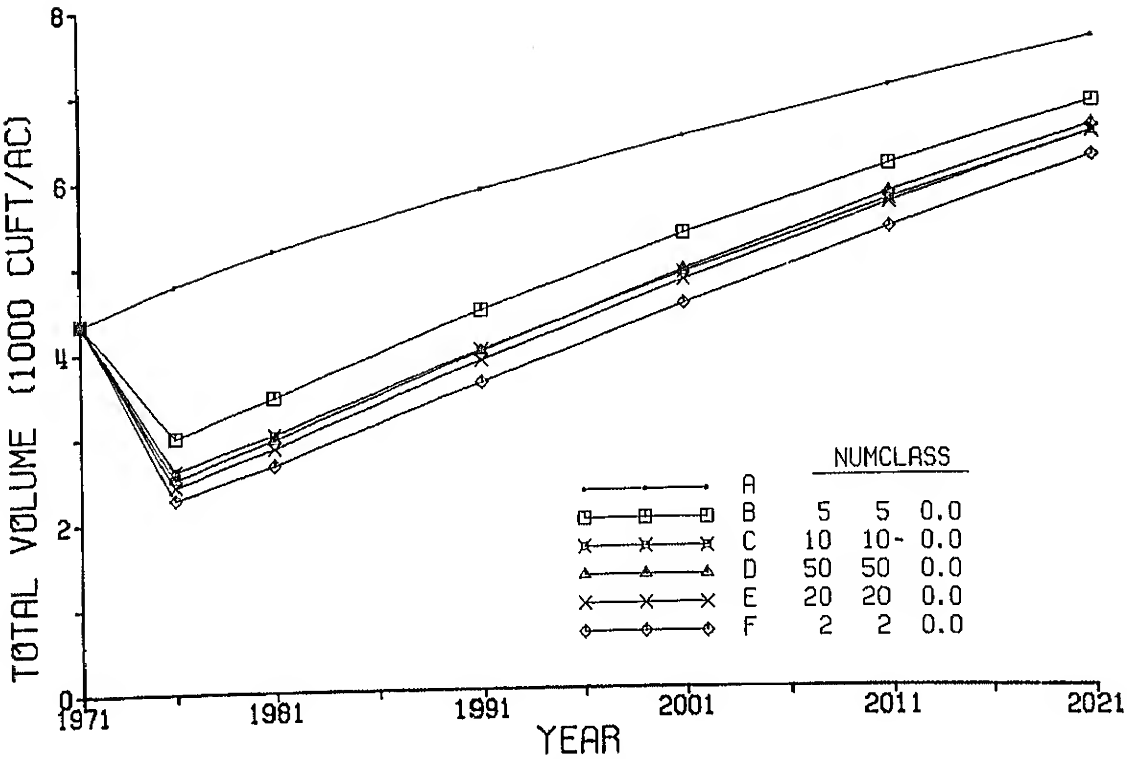

Figure 19.—Simulated volume development resulting from varying the number of tree classes to be created by exclusively using the successive halving algorithm (parameter 3 on the NUMCLASS keyword equals 0.0).

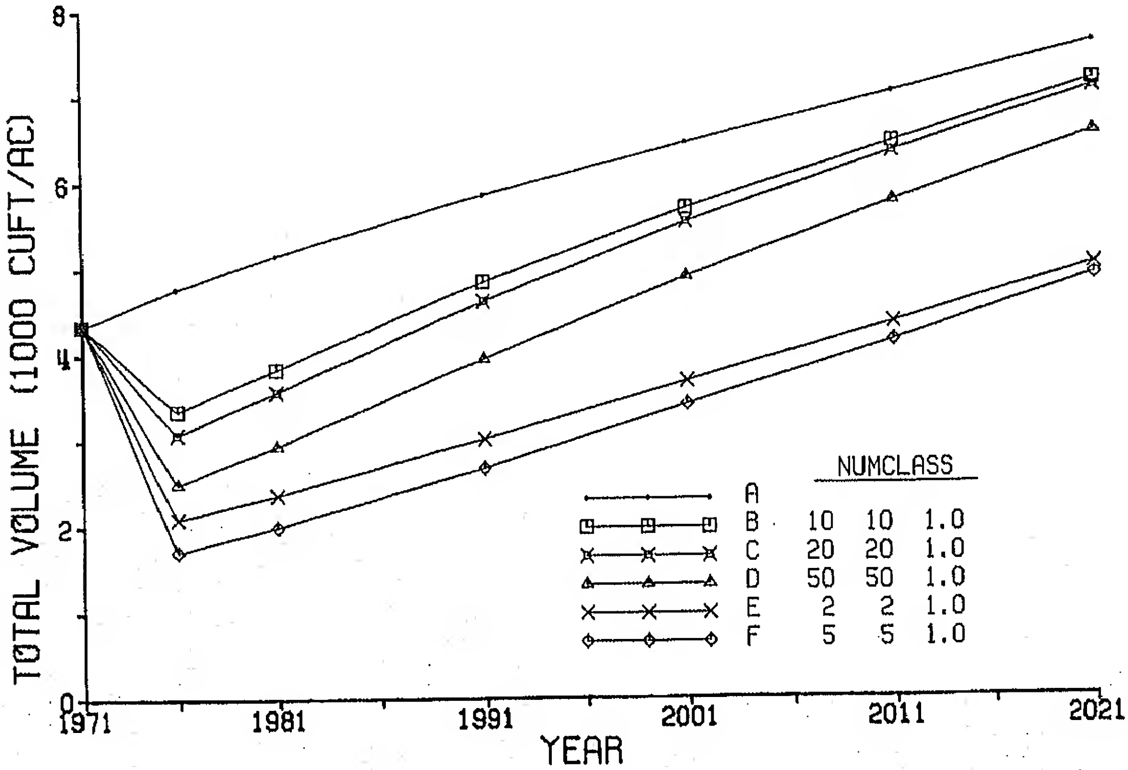

Figure 20.—Simulated volume development resulting from varying the number of tree classes to be created by exclusively using the maximum difference algorithm (parameter 3 on the NUMCLASS keyword equals 1.0).

An indication of the variability associated with the random larval allocation option is illustrated in figures 21 and 22. In figure 21, an average of 14 first instar larvae were randomly allocated to each tree class, with a standard deviation of 2 larvae; in figure 22 the standard deviation was increased to 8 larvae. Only the seeds of the random number generator were varied for the groups of simulations displayed in figures 21 and 22. As expected, the variability in simulated volume increases with the standard deviation of the distribution that the random number generator is being used to produce. Keep in mind that the default biomass option (4) contains an additional source of random variation in figures 21 and 22, as does the algorithm for assigning top-kill damage to individual trees.

When working with a simulation model containing varying degrees of random variability, there is always a risk that one simulation from a given set of initial conditions may be atypical. A good way to deal with this random variability is to generate replicate simulations (varying only the random number seeds) until the mean of the variable of interest (total volume over time in the examples in this section) is determined with acceptable accuracy; the user must of course consider the trade-off between the increase in both cost and precision to be obtained from additional replicate simulations in determining what level of accuracy is acceptable. An even better way to deal with the variability in the simulated system is to consider both the estimated mean and variance of the variable of interest in decision-making. For example, output from replicate runs of the simulation model can be used to estimate the probability that a given critical value (say, 4,000 ft^3/acre lost) will be exceeded in deciding whether or not to apply a control measure.

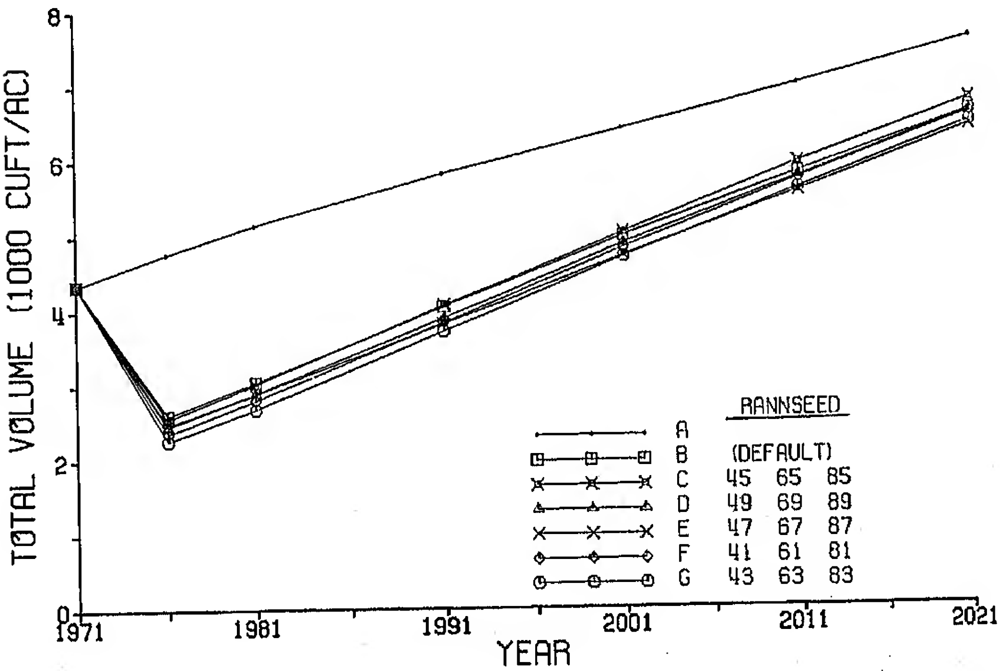

Figure 21.—Simulated volume development resulting from varying the sequence of random numbers used by the tussock moth related routines in the combined model. First instar larvae were allocated randomly to tree classes with an average of 14 and a standard deviation of 2 larvae.

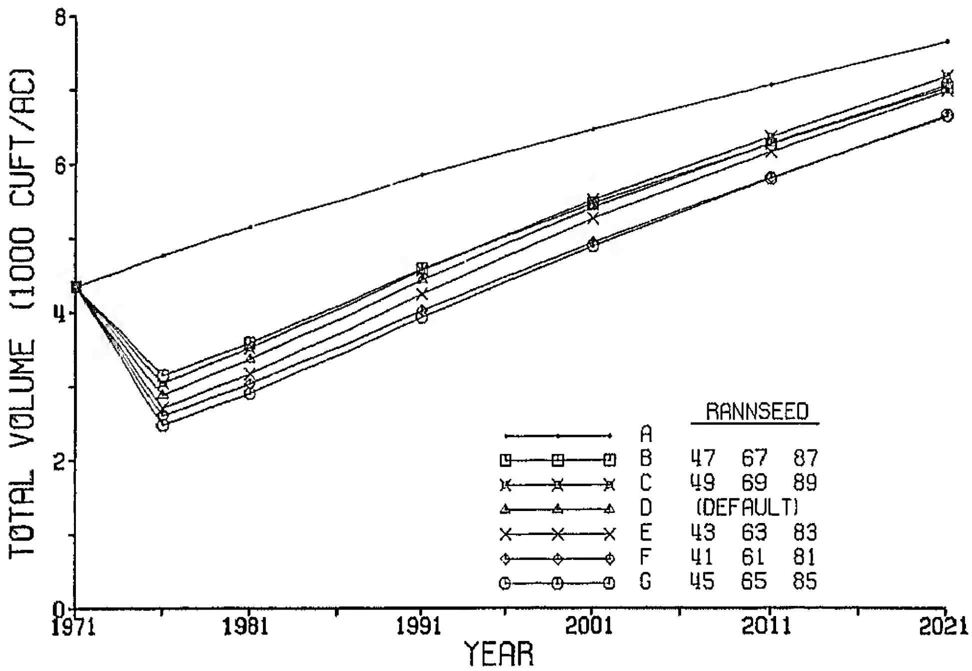

Figure 22.—Simulated volume development resulting from varying the sequence of random numbers used by the tussock moth related routines in the combined model. First instar larvae were allocated randomly to tree classes with an average of 14 and a standard deviation of 8 larvae.

Implications for Modeling Repeated Outbreaks

The portion of the Combined Model where unpredictable variation is most evident is in the algorithms that stochastically control the timing and occurrence of outbreaks (see the RANSCHED, RANSTART, and PROBMETH keywords). To illustrate (fig. 23), consider the following simulation. Regional outbreaks were scheduled with a probability of occurrence of 0.1, given that a 30-year waiting time had elapsed since the last regional outbreak. Whether or not the subject stand would be included in a regional outbreak was also determined stochastically, based on the stand's susceptibility to tussock moth. First instar larvae were allocated randomly to the tree classes (average = 14, standard deviation = 2); note that long-term larval density was held constant (between-outbreak standard deviation = 0.0 larvae). Default values were used for all other keywords and parameters. Five simulations were run; the first (fig. 23, curve B) used the default seeds for the random number generator, and the next four (fig. 23, curves C-F) used different random number generator seeds.

It is clear from figure 23 that the variability associated with this stochastic outbreak option is immense. Furthermore, it is quite unlikely that any given simulation using these same initial conditions could be called typical. If one is interested in estimating expected volume development over time resulting from these initial conditions, then it is almost essential to calculate the "average outbreak" volume curve (G).

Figure 23 can also be examined in a different light. Recall that the large variability exhibited by curves B-F results from changing only the sequence of random numbers. It follows that any manipulation of the stand—no matter how minor—that in effect alters this sequence of random numbers may produce results comparable to reseeding the random number generator. Thus the projected yields for two stands that are very similar—but not identical—could be quite different if severe but infrequent stochastic outbreaks (such as in figure 23) are being simulated. The importance of replicating a given simulation with different random number seeds cannot be overemphasized, especially when using the stochastic outbreak feature.

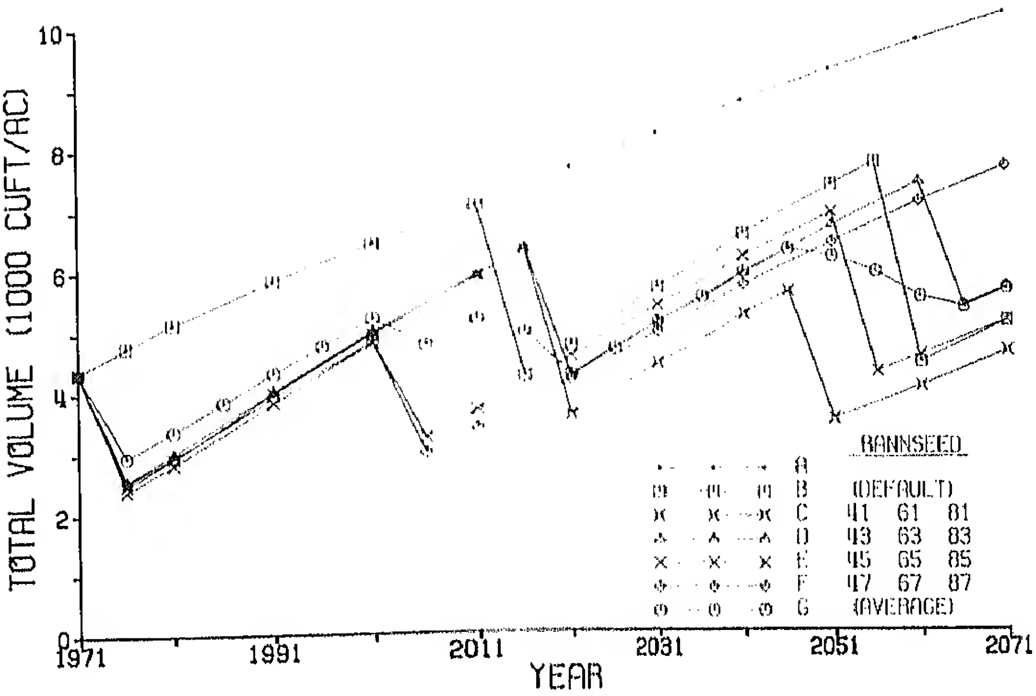

Figure 23.—Five replicates of simulated volume development resulting from varying the sequence of random numbers used by the tussock moth related routines in the combined model. Regional outbreaks were scheduled stochastically with a regional probability of outbreak of 0.1 given that a minimum of 30 years had elapsed since the last regional outbreak; whether or not the sample stand was included in the regional outbreak was also determined stochastically. The average outbreak curve G is obtained by averaging the five replicates (B-F).

Figure 24 illustrates six such average outbreak volume curves, with both the frequency and severity of the outbreaks being varied. As in the previous figure, the actual timing of outbreaks was stochastically determined by using the RANSCHED and RANSTART keywords, and larvae were randomly allocated to tree classes. Three levels of severity were simulated: an average of 4, 8, and 14 first instar larvae per tree class were allocated with a within-outbreak standard deviation of 2 larvae (roughly corresponding to light, moderate, and heavy severity, respectively). As in the previous figure, long term larval density was held constant (Field 4 on the RANLARVA keyword record was 0.0). For each of these levels of severity, both frequent and infrequent outbreaks were scheduled: the RANSCHED parameters for the frequent outbreaks were 7 years minimum time between outbreaks with a subsequent annual probability of regional outbreak of 0.3; the corresponding parameters for the infrequent outbreak schedule were 30 years and 0.1, respectively. The expected value of the time between outbreaks was thus 9-2/3 years for the frequent outbreak simulations and 39 years for the infrequent outbreaks. For each of the six combinations of outbreak severity and frequency, five replicates were simulated (by varying the seeds of the random number generator). Note that each curve graphed in figure 24 is the average of these five replicates. The default values for all other keywords were used.

For the range of conditions examined in this example, average volume lost (due to tussock moth) over time increased as either the severity (i.e., the number of larvae at the start of an outbreak) or the frequency of the simulated outbreak was increased; this is a rather predictable result. What is not very predictable, however, is the relative importance of frequency versus severity of outbreaks on long-term volume yields. It is quite difficult to make generalizations in this regard, for figure 24 contains both examples of frequency of outbreaks being a more important factor in explaining volume loss than the number of larvae at the start of an outbreak (compare cuves E and F) and vice versa (compare curves C and F).

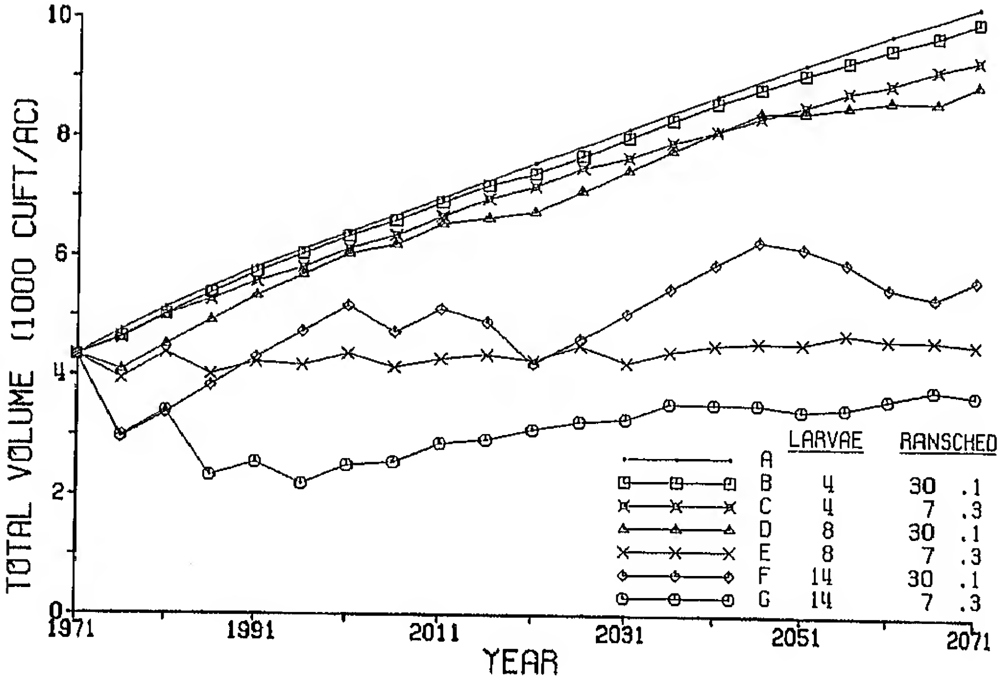

Figure 24.—Average simulated volume development resulting from varying the frequency of outbreaks for three different larval densities. Each outbreak curve (B-G) is the average of five simulations resulting from different random number sequences. The between-outbreak larval standard deviation was zero in these simulations.

Furthermore, there are probably many combinations of these factors that will produce the same amount of volume at a given age or time. For example, curves C and D are quite close together, even though outbreaks in curve D began with twice as many larvae as those in curve C, and the average interval between outbreaks is 30 years longer in curve D than in curve C. Such results have implications for hazard or risk rating systems. An accurate hazard rating scheme should obviously consider the long-term probability of outbreak as well as the likely severity of individual outbreaks. It is the joint effect of frequency and severity of outbreaks that determines the expected loss over time due to tussock moth.

The amount of variability associated with each of the average outbreak curves graphed in figure 24 decreased if either the severity of the simulated outbreaks was decreased or the frequency of the outbreaks was increased. Thus the average outbreak curve in figure 24 with the most variability is F; note that this curve is the same as curve G in figure 23.

An important point can be made regarding the simulations summarized in figure 24: a few of the curves are likely unrealistic. For example, it is highly unlikely that the combination of severe and frequent outbreaks averaged to produce curve G (and probably curve E) would ever occur in the same stand, although outbreaks have occurred as frequently in the Palouse Range and more severely in the Blue Mountains. Even though the same stand may be involved in repeated outbreaks, it is unlikely that such outbreaks would be equally severe and repeatedly start with the same larval density. The random larval allocation method contains an option that allows average larval density to vary from outbreak to outbreak. This option was used to produce figure 25: the between-outbreak standard deviation was set at 6.0 larvae (Field 4 on the RANLARVA keyword record) and all the simulations that were used to produce figure 24 were rerun. Thus figure 25 illustrates six average outbreak curves (again based on five replicates per curve) with both within- and between- outbreak severity (i.e., larval density) as well as outbreak frequency varying.

The major difference between figures 24 and 25 is that outbreak frequency is far more important when the between-outbreak larval standard deviation is moderately large (namely, 6 larvae in fig. 25). All three of the "frequent" outbreak curves in figure 25 (namely C, E, and G, with an expected interval between outbreaks of 9.7 years) were below the "infrequent" outbreak curves (B, D, and F, with 39 years the expected interval between out-

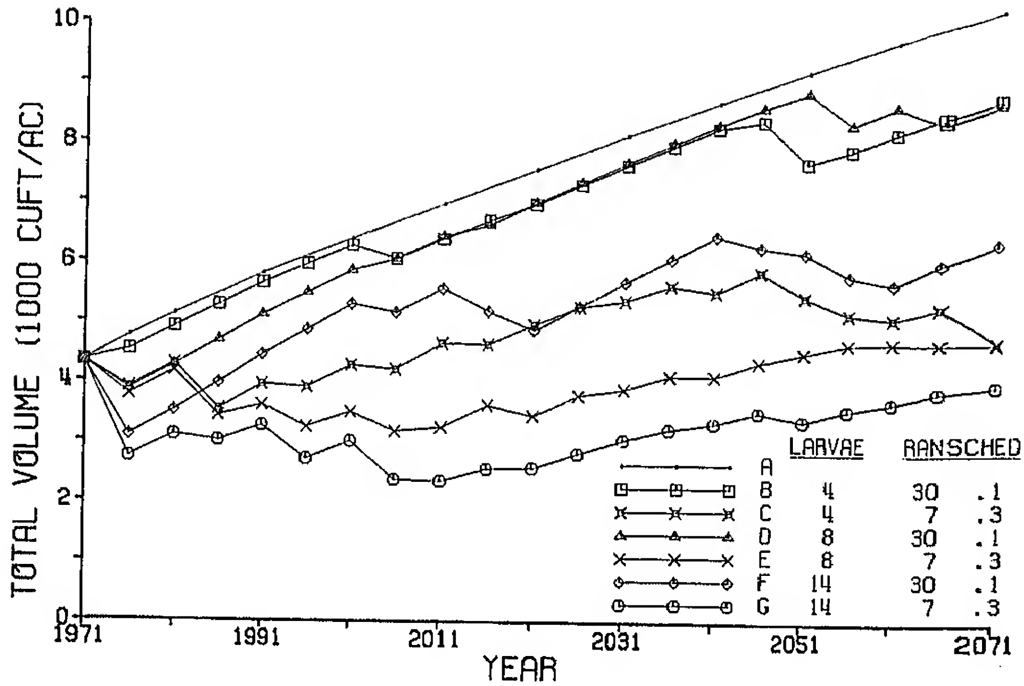

Figure 25.—Average simulated volume development resulting from varying both the frequency and the severity of the outbreaks. All simulations that produced figure 24 were rerun after raising the between-outbreak standard deviation to 6.0 larvae (Field 4 on the RANLARVA keyword record). Each outbreak curve (B-G) is the average of five simulations resulting from different random number sequences.

breaks). It may seem surprising that even curve C (frequent outbreaks with mean larvae = 4) is below curve F (infrequent outbreaks with mean larvae = 14); the reason is straightforward, however. With frequent outbreaks occurring four times as often as infrequent outbreaks, the chances of getting a severe outbreak (e.g., mean larval density = 14) are greater than 1 in 4 when the between-outbreak standard deviation equals 6 larvae, even though long-term mean density is only 4 larvae.

A final point suggested by both figures 24 and 25 concerns the use of expected yields (i.e., stand volume over time) in forest management planning. In an area where tussock moth has historically been a factor affecting stand development, it is probably overly optimistic to anticipate volume yields indicated by the "no outbreak" curve. Although it may be difficult to state with confidence which "outbreak" curve is most likely, almost all possibilities will predict less future volume than the "no outbreak" curve. The Combined Stand Prognosis/DFTM Outbreak Model has potential to reduce this bias associated with projecting future volume yields in stands susceptible to tussock moth.

The features of the Combined Model that allow both the frequency and severity of outbreaks to vary stochastically in multiple-outbreak simulations were added with hopes of making long-term projections more realistic. Unfortunately, there is little information indicating how the severity (i.e., number of larvae) of an outbreak is distributed over time, just as there is little—if any—information available describing the probability of stand outbreak for many different outbreak periods. Because of this dearth of knowledge, it was our objective to give the user considerable flexibility in stating assumptions regarding long-term interactions between the tussock moth and the stand being managed. The ultimate solution, of course, would be the development of a tussock moth population model that would be truly dynamic; this would eliminate the need for the Combined Model to predict the probability of outbreak, for the construct "outbreak" would then become an unnecessary artifact.

The numerous simulations graphed in this section were intended to serve merely as examples of model behavior rather than as definitive statements that will hold in all cases or for all stands, although some generalization from a number of the figures would be warranted. Our hope is that the potential user will have a greater appreciation for the scope and versatility of the Combined Model after viewing the numerous scenarios that can be simulated.

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